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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 15, 2004, 10:30:21; Search time 8.94737 Seconds (without alignments) 58.196 Million cell updates/sec Run on:

US-09-673-795-2 51 1 SLFEGIDIYT 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1	2260	$\circ$	028222 cercopithec		O9i8f9 oryzias lat	paracen		P36415 dictyosteli			sns	ratt			P22202 saccharomyc	_	bru							Q9u639 manduca sex	P02826 drosophila			_	P29843 drosophila		004967 sus scrofa	1877
SUMMARIES	ID	HS70 ONCVO	~	HS70 CHICK	HS71_CERAE	HS72_YEAST	HS71_ORYLA	HS74_PARLI	HS7A_CAEEL	1				HS71_RAT	HS71 YEAST	HS72 BOVIN	HS74_YEAST	HS71 MOUSE	HS70_BRUMA	HS70 ONCTS	HS70 PLEWA	HS70_NEUCR	HS72_SCHPO	HS70_XENLA	HS70_BLAEM	HS7D_MANSE			HS7X PIG	HS70 CERCA	HS7A_DROME		HS76 PIG	HS71_PUCGR
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RESULT 2 HS70\_PENCI ID \_HS70\_PENCI

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## 86.3 641   HSIA_RAT   P5506   ## 86.3 641   HSIA_RAT   P5506   ## 86.3 641   HSIA_RAT   P5525   ## 86.3 644   HSIA_CCRIGR   P5542   ## 86.3 644   HSIA_CCRIGR   P5542   ## 86.3 644   HSIA_CCRIGR   P5542   ## 86.3 646   HSIA_CRIGR   P51937   ## 86.3 649   HSIA_CRIGR   P5043   ## 86.3 649   HSIA_CRIGR   P5044   ## 86.3 649   HSIA_CRIGR   P6044   ## 86.3 649   HSIA	HSIA RAT HSTA RAT HSTT_MOUSE HS77_MOUSE HS77_FORDN HS71_SCHPO HS71_PICAN HS77_CRICAN HS77_CRICAN HS77_CRICAN HS77_CRICAN HS77_CRICAN HS77_CRICAN HS77_CRICAN HS77_CRICAN HS73_XEAST HS70_PARRE HS73_XEAST HS70_PARRE HS73_TAST HS70_PARRE HS73_TAST HS70_PARRE HS70_PARRE HS70_PARRE HS70_PARRE HS70_PARRE HS70_NEAGH SST OF A major IS70 (Pragment).  1, Chromadorea; Spiruriô Is from a filariasis-endem LS56(1989).  229-236(1989).  243-88; Frode and filariasis-endem LS6 (1980).  1s from a filariasis-endem LS6 (1980).  259-236(1980).  259-236(1980).  259-236(1980).  259-236(1980).  270-236(1980).  270-236(1980).  280-2447; B 1; Leng ARTIAL.  ARTIAL.  ARTIAL.  ARTIAL.  300-11; B 11 Leng Pred. No. 0.11; B 11 LENG B 11	HSIA RAT HSTA RAT HSTT_MOUSE HS77_MOUSE HS77_FORDN HS71_SCHPO HS71_PICAN HS77_CRICR HS77_CMOUSE HS77_CMOUSE HS70_PARER HS77_MOUSE HS70_PARER HS73_XEAST HS76_ERARE ALIGNMENTS	HSIA RAT HSTA RAT HSTT_MOUSE HS77_MOUSE HS77_FORDN HS71_SCHPO HS71_PICAN HS77_CRICR HS77_CMOUSE HS77_CMOUSE HS70_PARER HS77_MOUSE HS70_PARER HS73_XEAST HS76_ERARE ALIGNMENTS	HSIA RAT HSTA RAT HSTT_MOUSE HS77_MOUSE HS77_FORDN HS71_SCHPO HS71_PICAN HS77_CRICR HS77_CMOUSE HS77_CMOUSE HS70_PARER HS77_MOUSE HS70_PARER HS73_XEAST HS76_ERARE ALIGNMENTS	HSIA RAT HSTA RAT HSTA HUMAN HS72 LHUMAN HS72 LHUMAN HS72 LHUMAN HS72 LHUMAN HS73 LSCHPO HS71 SCHPO HS77 LHUMAN HS70 LMAST HS	P55063 rattuu P34931 homo on p16427 musum P5627 musum P5627 musum P5627 musum P5627 musum P5627 musum P63421 pichii p193421 pichii p19435 carchi a major immunogen in a maisis-endemic area.";  an T.V.;  b spirurida; Filarioidea;  is a major immunogen in a maisis-endemic area.";  produced through a collate ariasis-endemic area.  produced through a collate of forcem as its content is in a major immunogen in a maisis end the EMBL outsether as its content is in a sits content is in a large by and for com as its content is in a large by and for com a http://www.isb-sib.ch/an  3 1; Length 322;  3 1; Length 322;  11; Indels 0; Gap	P55063 rattuu P34931 homo o P16267 muun P153627 muun P153627 muun P19373 cricel P11142 homo o P08109 muu m P87047 paracc P09435 sacchi amunogen in a mic area."; family. rough a collat he EMB1 outsu restrictions tent is in y and for com 'isb-sib.ch/an 'isb-sib.ch/an 'isb-sib.ch/an 'isb-sib.ch/an 'isb-sib.ch/an 'isb-sib.ch/an 'isb-sib.ch/an 'isb-sib.ch/an

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01-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Heat shock 70 kDa protein (HSP70).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJINE-883304452; PubMed=3017985; Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.; Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.; "Organization, nucleotide sequence, and transcription of the chicken
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDINE=97351908; PubMed=9208190;
Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
Wholecular cloning and expression of a Penicillium citrinum allergen with sequence homology and antigenic crossreactivity to a hsp 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
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                                                                                                                                                                                                                                                                                                                                                  human heat shock profein.";

Clin. Bxp. Allergy 27:682-690(1997).

-1. ALLENGEN: Gauses an allergic reaction in human.

-1. SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 1; Length 503; Pred. No. 0.17;
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                                        16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Heat shock 70 kDa protein (Allergen Pen c 19) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55125 MW; B7433C11FAEA1320 CRC64;
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Pfam; PF00012; HsP70; 1.
PRINTS; PR00301; HsP70; 1.
PROSTIE; PS00297; Hsp70; 1.
PROSTIE; PS00239; HsP70 1; PARTIAL.
PROSTIE; PS01039; HSP70 2; 1.
PROSTIE; PS01036; HSP70 3; 1.
ATP-binding; Chaperone; Heat shock; Allergen.
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                      Created)
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90.0%;
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                      (Rel. 40, C
(Rel. 40, I
(Rel. 42, I
                                                                                                                               Penicillium citrinum.
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J. Biol. Chem
                      16-OCT-2001
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P08106;
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Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;
Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;
Inducible member of the hsp70 gene Which is salightly induced by heat is the main virus inducible member of the hsp70 gene family.";
FEBS Lett. 355:282-286(1994).
C. PERSISTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAX AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PRATICIPATE IN ALL THESE DROCESSES THROUGH THEIR ABILITY TO RECCONIZE NONATIVE CONFORMATIONS OF OTHER PROTEINS THEY BIND EXTENDED PEPTIDES SEGMENTS WITH A NET HYDROPHORIC CHARACTER EXPOSED BY POLYPEPTIDES COMPONENT BY THE A NET HYDROPHORIC CHARACTER EXPOSED BY POLYPEPTIDES COMPONENT BY THE A NET HYDROPHORIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.2%; Score 47; DB 1; Length 634; 90.0%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                   PIR, A25646; A25646.

HSSP; P08109; 1CKR.

InterPro; IPR001023; HSP70.

PEam; PR00121; HSP70; 1.

PRINTS; PR00301; HEATSHCK70.

PRODOM; PS00309; HSP70, 1.

PROSITE; PS00329; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                   EMBL; J02579; AAA48825.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 92.2
Best Local Similarity 90.0
Matches 9, Conservative
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TISSUE=Kidney;
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MEDLINE=95203288; PubMed=7895733;
Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B. Volpe T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                             Electrophoresis 15:1466~1486(1994).
                                                                                                                                                                            database."
             RANGE SEE STANDER 
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STRAIN=S288c / AB972;

MEDLINE=97131267; PubMed=9169871;

MEDLINE=97131267; PubMed=9169871;

MEDLINE=97131267; PubMed=9169871;

Benes V., Brueckner M., Delius H., Dubois E., Duestenhoeft A.,

Benes V., Brueckner M., Goffeau A., Hebling U., Heumann K.,

Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,

A houis E.J., Messenguy F., Mewes H.-W., Mioosga T., Moestl D.,

Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,

Portecelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,

Scharfe M., Schorens B., Scholler P., Schwager C., Schwarz S.,

Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,

Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,

Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIIRE=97197984; PubMed=9046100; Purnelle B., Goffeau A.; Purnelle B., Goffeau A.; "The sequence of 32kb on the left arm of yeast chromosome XII reveals six known genes, a new member of the seripauperins family and a new ABC transporter homologous to the human multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Slater M.R., Craig B.A.;
"The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-001-1989 (Rel. 11, Created)
10-001-1994 (Rel. 30, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Heat shock protein SA2.
SSA2 OR YLL024C OR L0931.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Fungi, Ascomycota, Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                 PRINTS: PRO0301; HEATSHCKYO.
PRODOM; PD000089; HSp70; 1.
PROSITE; PS00239; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 638 AA
or send an email to license@isb-sib.ch)
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                                        EMBL; X70684; CAA50019.1; -. PIR; S31766; S31766.
                                                                                                                         HSSP; P08107; 1HJO.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
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Best Local Similarity 90.00
Best Local 9, Conservative
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H872 YEAST

AC P10592;
DT 01-UUL-1989
DT 01-OCT-1994
DT 01-OCT-1994
DT 01-OCT-1984
DT 01-OCT-1989
DT 01-OCT-1989
DT 01-OCT-1989
DT 01-OCT-1989
DE Heat shock p
SSA2 OR YLLO
OS SACCHATOMYCE
OC ENGARYCE; FRO
C ENGARYCE; FRO
C STRAINES288C
RX MEDLINE-8912
RA SIQUENCE FRO
RY MEDLINE-8912
RA MEDLINE-8719
RA SIQUENCE FRO
C STRAINE-8288C
RX MEDLINE-9719
RA The SEQUENCE FRO
STRAINES288C
RX MEDLINE-9719
RA The SEQUENCE FRO
RY SEQUENCE FRO
RY MEDLINE-9713
RA SEQUENCE FRO
RY SEQUENCE FRO
RY MEDLINE-973
RA HEUSS-NEIZE
RA LOUIS E.J.,
RA HEUSS-NEIZE
RA UNDELWEGELS
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                                                                 Norbeck J., Blomberg A.; "Protein expression during exponential growth in 0.7 M NaCl medium of Saccharomyces cerevisiae.";
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GO:0009277; C:cell wall (sensu Fungi); IDA.
GO:0005737; C:cellwall DA.
GO:00003739; C:cytoplasm; IDA.
GO:000373; F:heat shock protein activity; IMP.
GO:0006457; P:protein folding; IMP.
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PROSITE; PS00329; HSP70 2; 1.
PROSITE; PS01036; HSP70 3; 1.
Heat shock; ATP-binding; Multigene family; Acetylation; INIT_MET 0
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; 23BDDD120C194912 CRC64;
                                                                                                                                       FEMS Microbiol. Lett. 137:1-8(1996).
SEQUENCE OF 186-195.
STRAIN-ATCC 38531 / Y41;
MEDLINE-97089742; PubMed=8935650;
                                                                                                                                                                             ACETYLATION, AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BMBL; X12927; CAA31394.1; -.
BMBL; Z73129; CAA97472.1; -.
BMBL; X97560; CAA6167.1; -.
BMBL; S20139; S20139.
HSSP; P19120; 3HSC.
GermOnline; 142019; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GermOnline; 142019; -.
SWISS-2DPAGE; P10592; YEAST.
COMPLUYEAST-2DPAGE; P10592; -.
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ProDom; PD000089; Hsp70; 1.
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Best Local Similarity
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EMBL; M18540; AAA28078.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLFEGIDIYT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
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HS7A_CAEEL
ID_HS7A_C
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                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Heat shock 70 kDa protein 1 (HSD70-1).
Oryzias latipes (Medaka fish) (Japanese ricefish).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Releostei; Neoteleostei;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE=93077053; PubMed=1339375; Sconzo G., Scardina G., Ferraro M.G.; Sconzo G., Scardina G., Ferraro M.G.; "Characterization of a new member of the sea urchin Paracentrotus lividus hsp70 gene family and its expression."; Gene 121:553-358(1992).
-i. SIMILARITY: Belongs to the heat shock protein 70 family.
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                                                                                                                                                                                                                                                                                                                                 LEGUENCE FROM N.A.
Naruse K., Sakuragi M.;
Naruse K., Sakuragi M.;
"Medaka HSP70 gene cloning.";
Submitted (JUL.2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
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Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.2%; Score 47; DB 1; Length 639; 90.0%; Pred. No. 0.22;
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Pham; PP00012; HSP70; 1.
PRINTS; PR000301; HSP70; 1.
PROSITE; PS00297; HSP70 1; 1.
PROSITE; PS003297; HSP70 1; 1.
PROSITE; PS01036; HSP70 2; 1.
PROSITE; PS01036; HSP70 3; 1.
ATP-binding; Heat shock; Multigene family.
ATP-binding; Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -874 PRLI STANDARD; PRT; 639 AA. 206248; 01-JWN-1994 (Rel. 29, Created) 01-JWN-1994 (Rel. 29, Last sequence update) 01-JWN-1994 (Rel. 29, Last annotation update) Heat shock 70 kDa protein IV (HSP70 IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF286875; AAF91485.1; -. HSSP; P08109; 1CKR.
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                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLFEGIDEYT 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                              ORYLA
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                       HS71 ORYLA ID HS71 ORY AC Q918\overline{F}9;
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    RESULT 6
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Rhabditidae, Peloderinae, Caenorhabditis.
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Snutch T.P., Heschl M.F.P., Baillie D.L.;
"The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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-!- SIMILARITY: Belongs to the heat shock protein 70 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.2%; Score 47; DB 1; Length 639; 90.0%; Pred. No. 0.22;
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HIGHERT: PR001023; HSP70.
PFAM: PP000121; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
ProDom: PD000089; HSP70; 1.
PROSITE: PS00329; HSP70; 1.
PROSITE: PS00329; HSP70; 1.
PROSITE: PS00329; HSP70; 1.
PROSITE: PS01336; HSP70; 3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
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01-MAR-1989 (Rel. 10, Last sequence update)
01-EBB-1994 (Rel. 28, Last annotation update)
Heat shock 70 kDa protein A.
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                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLIALID: FUNCHERE R.A., CONDECALLS J. S.;

Eddy R.J., Sauterer R.A., Condecalis J.S.;

"Aginactin, an agonist-regulated F-actin capping activity is associated with an Hac70 in Dictyostelium.";

J. Biol. Chem. 268.23267-23274(1993).

-I. FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN FINDING PROTEIN CAP32/34, ACTS AS A CHAPERONE BY STIMULATING THE REPOLDING OF DENATURATED CAP32.

-I. SUBCELLULAR LOCATION: Cytoplasmic. Found in F-actin-rich regions of the call cortex and call protrusions.

-I. DEVELOPMENTAL STAGE: Heat shock cognate proteins are expressed constitutively during normal development.

-I. SIMILARITY: Belongs to the heat shock protein 70 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94008983; PubMed=8404847;
Haus U., Irommler P., Fisher P.R., Hartmann H., Lottspeich F.,
Noegel A.A., Schleicher M.;
"The heat shock cognate protein from Dictyostellum affects actin
polymerization through interaction with the actin-binding protein
                                                                  .
0
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   DB 1; Length 640;
0.22;
                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
MCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Score 47; DB 1
Pred. No. 0.22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                   640 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat shock cognate protein (Aginactin). HSPB OR HSC70.
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MEDLINE=94043116; PubMed=8226849;
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PIRL; A4847.1 A4847.
PIR; A4847.
PIR; S37394; S37394.
HSSP; P19120; 3HSC.
SWISS-2DPAGE; P36415; DICTY.
DictyBase, DB0001837; HSP70.
InterPro; IPRO0122; HSP70. IPRO1125; PS00012; HSP70. IPROS115; PS000303; HSP70. IPROS115; PS00303; HSP70. IPROS115; PS00303; HSP70. IPROS115; PS00323; HSP70. IPROS116; PS00323; HSP70. IPROS16; PS00323; PS
                      90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 12:3763-3771(1993).
                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                        287 SLFEGIDFYT 296
                                                                                                                  1 SLFEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Chaperone CONFLICT 1 29
                         Best Local Similarity
Matches 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Query Match
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-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREXISTENT PROTEINS AGAINST AGRAGATION AND MEDIATE THE FOLIDING OF UNBLY TRANSLATES AGAINST AGRAGATION AND MEDIATE THE FOLIDING OF UNBLY TRANSLATED POLYEPPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE EMDOPLASMIC RETICULM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONMATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARRACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBERANE TRANSLOCATION, OR FOLLOWING
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gutierrez J.A., Guerriero V.; "Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-shock protein (Hgp70) mimics Hsp70 isoforms from tissues."; Biochem. J. 305:197-203(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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Grosz M.D., Skow L.C., Stone R.T.;
"An Alul Polymorphism at the bovine 70 kD heat-shock protein-1
(HSP70-1) locus.";
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                                                                                                                                                                                                                                                               Length 640;
                                                                                                                                                                                                                                                                                                                    1; Indels
N -> T (IN REF. 2).

R -> A (IN REF. 2).

R -> A (IN REF. 2).

S -> A (IN REF. 2).

V -> A (IN REF. 2).

V -> A (IN REF. 2).

Y -> D (IN REF. 2).

ZE6BDC2DB96A9FSD CRC64;
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                                                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                            47;
No. (
                                                                                                                                                                                                                                                         Score Pred. 1
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TISSUE-Skeletal muscle;
MEDLINE-95126904; Pubmed-7826329;
                                                                                                                                                                                                    70499 MW;
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SEQUENCE OF 212-641 FROM N.A.
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                                                                                                                                                                                                                                                         92.28;
                                                                                                                                                                                                                                                                                    90.06;
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                                                                                                                                                                                                                                                                                                                 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        284 SLFEGIDFYT 293
                                                                                                                                                                                                                                                                                                                                                                      1 SLFEGIDIYT 10
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                                                                                                                                                                                                                                                                                 Local Similarity
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NCBI_TaxID=9913;
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CONFLICT
CONFLICT
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                      Query Match
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HS71_BOVIN
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Matches
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PIR, A29160, A29160.
PIR, A45871, A45871.
PIR, I59139, I59139.
PIR, I79540, I79540.
PDB, 1HJO, 21-OCT-98.
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (HSPAIA AND HSPAIB).
Shina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229, 817bp genomic DNA of 6p21.3 HLA class I region.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=86016721; PubMed=3931075;
Hunt C., Morimoto R.L.;
"Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";
Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (HSPAIA AND HSPAIB).

Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,

Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,

Lasky S., Hood L.,

"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91055806; PubMed=1700760;
MILDER C.M., Campbell R.D.;
"Structure and expression of the three MHC-linked HSP70 genes.";
Immunogenetics 32:242-251(1990).
                                                                                                                                                0;
    HSP1 HUMAN STANDARD; PRT; 641 AA.
P08107; P19790; Q9UQLD; Q9UQMO;
01-AUG-1988 (Rel. 08, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-007-2003 (Rel. 42, Last annocation update)
Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1).
(HSPA1A OR HSPA1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                         286 SLFEGIDFYT 295
                                                                                                                                                                     1 SLFEGIDIYT 10
                                                                                                                                                                                                                                                                                                                      (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                           Query Match
                                                                                                                                                 Matches
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PARTITION OF NOTICE TO THE STATES A. GARTIA A. M. Gibbs R.A.,

RADIATION OF M. WORLEY R.C., FIRE STATES A. M. Gibbs R.A.,

RADIATION OF M. Worley R.C., Fire M. M. Greengers B.J., L. M. Gibbs R.A.,

MAILTING W. W. Medan A., Young A.C., Shavchenko Y. Fouffact G.C.,

MAILTING W. W. Medan A., Young A.C., Shavchenko Y. Fouffact G.C.,

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READ CALLEST A. Durham I., Trowdelle J., Campbell R.D.,

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Gaps

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Score 47; DB 1; Length 641; Pred. No. 0.22; 0; Mismatches 1; Indels

92.2%;

Query Match Best Local Similarity

337 342 353 356

333 333 344 354

STRAND HELIX HELIX TURN 9; Conservative

Matches

1 SLFEGIDIYT 10

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R SWISS-STANDAR, PROTO, HUMAN.

R Genew, HRON: 2223; HSFALB.

R MIN, 140550, 7.

R MIN, 14050, 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete nucleotide sequence of a porcine HSP70 gene.";
Immunogenetics 35:286-289(1992).

-!-FUNCTION: In cooperation with other chaperones, Hsp70s stabilize preexistent proteins against aggregation and mediate the folding of newly translated polypeptides in the cytosol as well as within organelles. These chaperones participate in all these processes through their ability to recognize nonative conformations of other proteins. They bind extended peptide segments with a net hydrophobic character exposed by polypeptides during translation and membrane translocation, or following stress-induced damage.
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE-92175874; PubMed=1339404;
Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
Bouquet Y.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 0.22;
0; Mismatches 1; Indels
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PIR; 335718; 335718.
HSSP; P08107; 11470.
InterPro; 12R001023; HSP70; 1.
PRINTS; PR00301; HSP70; 1.
PROSITE; PS00297; HSP70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01329; HSP70_2; 1.
PROSITE; PS01329; HSP70_3; 1.
ATP-binding; CApperone; Heat shock; Multigene family.
SEQUENCE 641 AA; 70083 WW; FE77BE20A03E0A33 CRC64;
                                                                                                       RESULT 12
HS71 PIG STANDARD; PRT; 641 AA.
AC P34930;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DF Heat shock 70 kDa protein 1 (HSP70.1).
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       286 SLFEGIDFYT 295
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Matches 9; Conserv
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                            MEDLINE-94096443; PubMed-8271311;
Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
Massa S.M., Sharp F.R.;
"cDNA cloning and expression of stress-inducible rat hsp70 in normal
                                                                                                                                                                                                                                                               STRAIN=LEW.1W/GUN;
MEDLINE=95012453; PubMed=7927536;
Walter L., Rauh R., Guenther B.;
"Comparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:325-330(1994).
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAINESPIRELLIVER; STRAINESPIRER, PUDMALEY; MEDLINESPIRER, PubMed=8086479; Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.; "Cloning, nucleotide sequence and expression of rat heat inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L16764; AAA17441.1; -...
EMBL; X77208; CAA54423.1; -...
EMBL; X77207; CAA54422.1; -...
EMBL; X74271; CAA55422.1; -...
EMBL; X74271; CAA55422.1; -...
PIR; I54542; I54542.
InterPro; IPRO101023; HSP70.
R PROBUJT; PRO01012; HSP70; 1...
R PROSITE; PS00297; HSP70.1; 1...
R PROSITE; PS00297; HSP70.1; 1...
R PROSITE; PS01036; HSP70.2; 1...
R PROSITE; PS01036; HSP70.2; 1...
R PATP-binding; Chaperone; Heat shock; Multigene family.
CONFLICT 71 72 KR -> NG (IN REF. 3).
                                           007439; P42853;
01-FBB-1995 (Rel. 31, Created)
01-FBB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Heat shock 70 kDa protein 1/2 (HSP70.1/2).
Hap70-1 AND HSP70-2.
Rattus norvegicus (Rat).
                                   641 AA
                                   PRT;
                                                                                                                                                                                                                                 J. Neurosci. Res. 36:325-335(1993)
[2]
SEQUENCE FROM N.A.
                                   STANDARD;
                                                                                                                                                                                                                          and injured rat brain.
                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=10116;
                         HS71 RAT
ID HS71 RAT
               RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=22867 / AB972;
MEDLINE=95028152; PubMed=7941740;
MEDLINE=95028152; PubMed=7941740;
MEDLINE=95028152; PubMed=7941740;
MEDLINE=95028152; PubMed=7941740;
Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
"Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the 42 kbp SPO7-CENI-CDC15 region.";
Yeast 10:535-541(1994).
                                                                                                                                                                 Gaps
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ACETYLATION.
Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Slater M.R., Craig E.A.; "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae."; Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 590-641 FROM N.A.
MEDLINE=85087943; PubMed=6096826;
Ogden R.C., Lee M.-C., Knapp G.;
"Transfer RNA splicing in Saccharomyces cerevisiae: defining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender F
Volpe T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                              ·.
                                                                                                    92.2%; Score 47; DB 1; Length 641; 90.0%; Pred. No. 0.22; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases
227 D -> H (IN REF. 2 AND 3).
108 G -> A (IN REF. 3).
70163 MW; D02D96751C868583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-UTL-1999 (Rel. 11, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last amotation update)
Heat shock protein SSA1 (Heat shock protein YG100).
SSA1 OR YALO0SC.
                                                                                                                                                                                                                                                                                                                                                                                                           641 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 12:9367-9382(1984).
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FEMS Microbiol. Lett. 137:1-8(1996)
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Electrophoresis 15:1466-1486(1994)
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MEDLINE=97089742; PubMed=8935650;
Norbeck J., Blomberg A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288c;
MEDLINE=95203288; PubMed=7895733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89128457; PubMed=2644626;
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                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                        286 SLFEGIDFYT 295
  227
                                                                                                                                                                                                                         1 SLFEGIDIYT 10
                                                                                      Query Match
Best Local Similarity
     227 2
408 4
641 AA;
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BMR EMBL; X22015; AAC04952.1; ALT_SEQ.

BR FIR; A3449; HHRYA1.

BR HSSP; P19120; 318C.

Germonline; 138348; -.

Germonline; 138348; -.

BR SWISS-2DPAGE; P10591; -.

BR GO; GO:000273; C:Cytcplasm; IDA.

GO; GO:000537; C:Cytcplasm; IDA.

GO; GO:000537; C:Cytcplasm; IDA.

GO; GO:000537; C:Cytcplasm; IDA.

GO; GO:000537; F:ATPase activity; IDA.

GO; GO:000537; F:ATPase activity; IDA.

GO; GO:0006619; P:RAPCase activity; IDA.

GO; GO:0006619; P:RAPCase activity; IDA.

GO; GO:0006619; P:RAPCase activity; IDA.

GO; GO:0006619; P:Protein folding; IDA.

GO; GO:0006619; P:Protein folding; IDA.

GO; GO:0006619; P:RP-dependent cotranslational membrane targ. .; IDA.

BR FAMPS; PROGOT; HSAPCO. 1.

BR PROSITE; PSC0329; HSAP70.1.

BR PROSITE; PSC0329; HSAP70.1.

BR PROSITE; PSC0329; HSP70.2; I.

RR PROSITE; PSC0329; HSP70.2; I.

BR PROSITE; PSC0329; HSP70.2; I.

RR PROSITE; PSC0329; HSP70.3; I.

RR PROSITE; PSC0329; HSP70.2; I.

RR PROSITE; PSC0329; HSP70.3; I.

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0
Volpe T., Warner J.R., McLaughlin C.S.,
Submitted (SEP-1994) to Swiss-Prot.
-!-FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE
ATP-DEPRINDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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Best Local Similarity 90.00,
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NCBI_TaxID=9913;
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H872_BOVIN
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AC 027965B
DT 01-NOV
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DF 10-NOV
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THEY CALLE TITLUS TITLUS TO A COPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANILLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROFESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.

-!- INDUCTION: By heat shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                               TISSUE-Liver;
MEDLINE-9407117; PubMed-8249428;
MEDLINE-9407117; PubMed-8249428;
Kowalski J., Gilbert S.A., van Drunen-Littel-Van den Hurk S.,
van den Hurk J., Babiuk L.A., Zamb T.J.;
"Heat-shock promoter-driven synthesis of secreted bovine herpesvirus
glycoproteins in transfected cells.";
Vaccine 11:1100-1107(1993).
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Grosz M.D., Skow L.C.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIGHLEUS, AEROLIZ, HESP70; 1
PEAM; PF00121; HESP70; 1
PRINTS; PR00301; HESP70; 1.
PROSITE; PS001301; HSP70; 1.
PROSITE; PS001329; HSP70 2; 1.
PROSITE; PS01036; HSP70 2; 1.
PROSITE; PS01036; HSP70 2; 1.
APP-binding; Chaperone; Heat shock; Multigene family.
SEQUENCE 641 AA; 70228 MW; 229C19EEBBF610DF CRC64;
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90.0%; Pred. No. 0.22;
iive 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U02892; AAA03451.1; -. EMBL; M98023; AAA30568.1; -. PIR; 145911; 14591. HSSP; P08107; 1400. InterPro; IPRO01023; HSP70.
                                                                                                            SEQUENCE OF 1-28 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
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Best Local Similarity
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alopias vul alopias sup

cetorhinus

alopias sup megachasma

mitsukurina lamna ditro

cetorhinus odontaspis odontaspis odontaspis

megachasma

lamna ditro ditro alopias pel pseudocarch

08 JHR Z
08 JHR Z
08 JHR B
08

08jhr8 08jhr3 08jhr6 08jhr6 08jhr9 08jhr1 08jhr1 08jhr1 08jhr9 08jhr9 08jhr6 08jhr6 08jhr6 08jhr6 08jhr6 08jhr6 08jhr6 08jhr7 08jhr7 08jhr7 08jhr7 08jhr7 08jhr7

alopias pel alopias pel pseudocarch odontaspis

odontaspis

alopias sup alopias vul odontaspis mitsukurina alopias pel pseudocarch

Q8jhr9 Q8jhr3 Q8jht2 Q8jhp2 Q8jhs5 Q8jhn5 J

Q8JHS5 Q8JHN5

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639 AA;
                                                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A.
Yamashita M.;
                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding
SEQUENCE
Q8UWM9;
                                                                                                                                                                                                               08UWM9
                                                                                                                                                                                                    RESULT 1
Q8UWM9
                                                                                                                                                                                                                     Q9u667 littorina p
Q9u669 littorina s
Q9u669 littorina s
Q9u669 littorina p
Q9u666 littorina p
Q9u666 littorina p
P81159 aplysia cal
Q90520 oncorhynchu
Q90520 oncorhynchu
Q90530 encorhynchu
Q81m8 cetorhinus
Q63718 rattus ratt
Q63718 rattus ratt
Q831ha gesudocarch
Q81hs0 alopias sup
Q81hs0 alopias sup
                                                                                                                                                                                                                                                                                                                                       Q8uwm9 xiphophorus
                                    September 15, 2004, 10:30:46; Search time 36.3158 Seconds (without alignments) 86.882 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                 1017041
   GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                    1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                         - protein search, using sw model
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Q9U665
Q9U665
Q9U665
Q9U666
Q9U666
Q9U668
Q9U668
Q9U689
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Gapop 10.0 , Gapext 0.5
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
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sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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51
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Match Length DB
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0 "Characterization of multiple members of the HSP70 family in platyfish Gaps Xiphophorus maculatus (Southern platyfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodoutiformes; Poeciliidae; Xiphophorus. 0; cultured cells.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-!- SINILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; AB062114; BAB7168.1;
GO; GO:000524; FATP binding; IEA.
InterPro; IPR01023; HSp70.
PEam; PR00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70. 94.1%; Score 48; DB 13; Length 639; 80.0%; Pred. No. 0.92; cive 2; Mismatches 0; Indels 70128 MW; 87382F59FDE5532C CRC64; 01-WAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) ALIGNMENTS ProDom; PD000089; Hsp70; 1. PROSITE; PS00297; HSP70 1; 1. PROSITE; PS00329; HSP70 2; 1. Conservative PRELIMINARY; Stress protein HSP70-2. 1 SLFEGIDIYT 10 Query Match Best Local Similarity Matches 8; Conserv 8

> Q63718 Q8JHN4 Q8JHS0 Q8JHP3

Q8JHM8

0;

Gaps

6

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Littorina plena (Black periwinkle).
Bukaryota, Metazoa, Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                            Littorina scutulata (Checkered periwinkle).
Bukaryota; Metazoa; Mollusca; Gaetropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Littorinoidea; Littorinidae; Littorinia.
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"Heat-shock genes in the heat-stressed genus Littorina.";
"Hohented (OcT-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (OcT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF191826; AAF12785.1; -..
GO; GO:000524; F:ATP binding; IEA.
InterPro; IPR00123; Hsp70.
Pfam; PF00012; HSP70; 1.
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        Score 47; DB 5; Length 153;
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Last annotation update)
                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                              0.3;
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                                                   0; Mismatches
                                Pred. No.
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01-MAY_2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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PROSITE, PS01036; HSP70.3; 1.
ATP-binding.
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          92.2%;
90.0%;
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Best Local Similarity 90..

Best Conservative
            Query Match 92.2
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                      80 SLFEGIDFYT 89
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NON TER
SEQUENCE
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Q9U665;
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Q9U669
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Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
                                                                                                                                                                                                                                             Littorina plena (Black periwinkle).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; Littorinimorpha; Littorinoidae; Littoriniae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                                       Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
submitted (COT-1999) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AP191828; AAF12787.1; -.
GO, GO:005524; F:ATP binding; IEA.
InterPro; IPR001023; HSP70.
PFam; PF00112; HSP70; 1.
PROSIDE; PS01036; HSP70; 1.
ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
"Heat-shock genes in the heat-stressed genus Littorina.";
submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL., AP191825, AAF12784.1;
-.
INTERPRO, 1825, AAF12784.1;
InterPro; IPRO01023; HSp70.
Fram, PRO01012; HSp70.
PROSITE, PS01036; HSP70.3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.2%; Score 47; DB 5; Length 146; 90.0%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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153 153
153 AA; 17352 MW; E29EE20C4CAF934D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 AA; 16607 MW; C3F3556A1AF438BB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat-shock protein (Fragment).
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                                                                                                     146 AA.
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288 SLFEGVDLYT 297
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146
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NON TER
NON TER 15
SEQUENCE 153
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SLFEGIDFYT 94
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Les 9; Conserv
                             SEQUENCE FROM N.A. Hohenlohe P.A.;
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Q9U668;
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Matches
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Q9U668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THEAL Shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
C -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; AR191824; AAF12783.1; -.
GO; GO:000524; FAFP binding; IEA.
InterPro; IPR001023; HSp70.
R Pfam; PR00310; HEATSHOCK70.
PRODOM; PR000129; HSP70; 1.
R PROSTIE; PR01036; HSP70; 1.
R PROSTIE; PR01036; HSP70; 1.
T NON TER 158 158
C SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;
                                                                                                                                                                                                                                ;
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Eukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
NCBI_TAXID=31221,
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Bukaryota, Metazoa; Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
                                                                                                                                                                                  92.2%; Score 47; DB 5; Length 157; 90.0%; Pred. No. 0.31; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.2%; Score 47; DB 5; Length 158; 90.0%; Pred. No. 0.31; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                   1 1
157 157
157 AA; 17834 MW; E8F743382B285EB2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat-shock protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                   158 AA
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                     PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; HSp70; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heat-shock protein (Fragment).
                                                                                                                                                                                  Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Pfam; PF00012; HSP70; 1
                                                                                                                                                                                                                                                                1 SLFEGIDIYT 10
                                                                                                                                                                                                                                                                                                         84 SLFEGIDFYT 93
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Best Local Similarity
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                                                                                ATP-binding.
                                                                                                 NON TER
NON TER
SEQUENCE
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Q9U666;
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Q9U671
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T. "Heat-shock games in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAWILY.
R EMBL; AF191829; AAF12788.1; -..
GO; GO: 0005524; F:ATP binding; IEA.
R InterPro; IPRO1012; HSP70.
R PRINTS; PRO0301; HEATSHOCK70.
R PRINTS; PRO0301; HEATSHOCK70.
R PROBON; PRO0089; HSP70; 1.
R PROSITE; PS01036; HSP70; 1.
R PROSITE; PS01036; HSP70; 3; 1.
R ATP-binding.
I NON TER 158 AA; 17891 NW; B41E5356BCECAD2F CRC64;
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Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
NCBI_TaxID=31219;
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158 158 17868 MW; D2ECE71042EC44CB CRC64;
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01.MAX-2000 (TrEMBLrel. 13, Last sequence update)
01.OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat-shock protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 AA.
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01-JUN-1998 (TrEMBLrel. 06, Created)
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ATP-binding.
1 1
NON_TER 158 158
SEQÜENCE 158 AA; 17868 MW;
                                                                                                                                                                                                                                                                                                                                                            Conservative
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Gaps

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Indels

Length 278;

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SEQUENCE FROM N.A.
MEDLINE=99284127; PubMed=10357235;
Lim E.H., Brenner S.;
Lim E.H., Brenner S.;
"Short-range linkage relationships, genomic organization and sequence comparisons of a cluster of five HSP70 genes in Fugu rubripes.";
Cell Mol. Life Sci. 55:668-678 (1999).
-I. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; Y08578; CAA69892.1; -.
HSSP; P19120; 3HSC.
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Blasmobranchii, Galeomorphii, Galeoidea, Lamniformes, Alopiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.2%; Score 47; DB 13; Length 367; 90.0%; Pred. No. 0.79;
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                                                                        278 278
278 AA; 30327 MW; E4C745DB5484C17A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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GO; GO:0003773; F:heat shock protein activity; IEA.
InterPro; IFR001023; HSp70.
PERM; FF00012; HSP70; 2.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                        92.2%; Score 47; DB 13; 90.0%; Pred. No. 0.58;
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PROSITE; PS00297; HSP70 1; 1.
PROSITE; PS01036; HSP70 3; 1.
ATP-binding; Heat shock.
NON TER 367 367
SEQUENCE 367 AA; 40406 MW;
           PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock.
NON_TER 1 1
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01-0CT-2002 (TrEMBLrel. 22,
01-0CT-2003 (TrEMBLrel. 25,
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Best Local Similarity 90...
9; Conservative
                                                                                                                         Query Match
Best Local Similarity 90.0.
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HSP70.
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                                                                                                                                                                                                                                                                      156 SLFEGIDFYT 165
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                                                                             NON TER
SEQUENCE
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MEDLINE-93077669; PubMed=1360013;

Kuhl D., Kennedy T., Barzilai A., Kandel B.;

"Long-term sensitization training in Aplysia leads to an increase in "Long-term sensitization training in Aplysia leads to an increase in the expression of BiP, the major protein chaperon of the BR.";

T. Cell BiOl. 119-1069-1076 (1992)

C. I. SINILARITY: BELONGY TOWITUSIZED IN A WIDE VARIETY OF CELLS.

EMBL; Z15039; CAA-78757.1; -...

BIR, B4261; B44261.

R PIR; B44261; B44261.

R OS GO: 0003773; Fiheat shock protein activity; IEA.

InterPro; IPR001023; HS970.

R PROSTIF; PR001029; HS970.

PRODM; PR000089; HS970.

R PROSTIF; PS01036; HS970.2; 1.

R PROSTIF; PS01036; HS970.2; 1.
                                                                        Aplysia californica (California sea hare).
Bukaryota, Metazoa; Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Heterobranchia, Euthyneura, Opisthobranchia; Anaspidea;
Aplysioidea, Aplysiidae, Aplysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Rainbow trout 70 kDa heat shock protein (Fragment).
Guochynchus mykiss (Rainbow trout) (Salmo gairdheri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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MEDITE=85036330; PubMed=6092938;
KCthary R.K., Jones D., Candido B.P.M.;
"70-kilodalton heat shock polypeptides from rainbow trout:
Characterization of CDNA sequences.";
Mol. Cell. Biol. 4:178-1791(1984).
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 5; Length 220; Pred. No. 0.45; 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24684 MW; FA8557F2BB85C37A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; K02549; AA49562.1; ---
PIR; 151344; 151344.
HSSP; P08107; 1H40.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003773; F:heat shock protein activity; IEA.
InterPro; IPR001023; HSP70.
Pfam; PR00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; HSP70; 1.
PROSITE; PS00329; HSP70.2; 1.
01-JUN-1998 (TrEWBLrel. 06, Last sequence update) 01-JUN-2003 (TrEWBLrel. 24, Last annotation update) Heat shock cognate 71 kDa protein (Fragment). HSC70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 SLFEGIDEYT 147
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Best Local Similarity
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Gaps

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Indels

us-09-673-795-2.rspt

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PRINTS; PR00301; HEATSHOCK70
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                                                                                                                                                                                                                                                                                                               Hsp70 protein (Fragment).
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Matches 9; Conservative
                                                                                                                                              PRELIMINARY;
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244 SLFEGIDFYT 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Alsu2;
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Q8JHN4;
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                                                                           RESULT 14
                                                                                                              Q8JHN4
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Bukaryota, Metacoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10117;
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"Cloning of CDNA for the rat inducible 70KD heat shock protein
(HSP40).";

Submitted (KOV-1993) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

R HSSP; PO8107; 1HJO.

GO; GO:0005524; F:ATP binding; IEA.

InterPro; IPR001023; HSP70.

R Pfam; PF00012; HSP70.

R PROSITE; PR00301; HZATSHOCK70.

PRODM; PD000089; HSP70.

R PROSITE; PS00329; HSP70.2; 1.

R PROSITE; PS01329; HSP70.2; 1.

M ATP-binding.

INON_TER 455 455

SEQÜENCE 455 AA; 50405 MW; 0F45F12CBA1E2971 CRC64;
                                                                                                                                                                    Martin A.P., Burg T.; "Perils of paralogy: Using Hsp70 genes for inferring organismal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,
                                                                                                                                                                                                                                                          Submitted (ARR-2002) to the BMBL/GenBank/DDBJ databases.

-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
BMBL, AFF02494; AAM5302.1; -.
GO, GO:0005234; F.APP binding; IEA.
InterPro; IPR010123; HSp70.
Pfam; PR00012; HSP70. 1.
PROSITE; PR00303; HSP70; 1.
PROSITE; PS00329; HSP70; 1.
PROSITE; PS00329; HSP70; 1.
ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.2%; Score 47; DB 13; Length 444; 90.0%; Pred. No. 0.97; 1: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 AA; 48889 MW; 7701945FBB99A2BA CRC64;
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19; Conserva
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Best Local Similarity
                                                                                         SEQUENCE FROM N.A.
                            NCBI_TaxID=57982;
                                                                                                                                                                                                                                        phylogenies.";
                                                                                                                                    STRAIN=Cema6;
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SEQUENCE
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                                                                                                                                                                                        Pseudocarcharias kamoharai.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Galeomorphii; Galeoidea; Lamniformes;
Pseudocarchariidae; Pseudocarcharias.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Alopiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                           Martin A.P., Burg T.; "Perils of paralogy: Using Hsp70 genes for inferring organismal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phylogenies.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; APS 0.488; APAMS 3196.1;
-- GO; GO:0005524; F:ATP binding; IEA.
InterPro; IPR001023; HSP70.
Pfam; PP00012; HSP70; 1.
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-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AFSO2452; AAM53160.1; -.
GO; GO:0005524; F:ATP binding; IEA.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.2%; Score 47; DB 13; Length 459; 90.0%; Pred. No. 1; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           459 AA; 50209 MW; 0D0055A45248652A CRC64;
                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Last sequence update)
Last annotation update)
459 AA.
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PROGOSO1; HEATSHOCK70.
ProDom; PD000089; HSP70; 1.
PROSITE; PS00129; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding. 1 1
NON_TER 1 1
NON_TER 459 AA; 50209 MW; C
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DR PROSITE; PS01029; HSp70; 1.

DR PROSITE; PS01029; HSp70_2; 1.

DR PROSITE; PS01036; HSp70_2; 1.

KW ATP-binding. 1

FT NON_TER 461 461

SQ SEQUENCE 461 AA, 50591 MW; 1A9ESB4BC41077FE CRC64;

Query Match

Best Local Similarity 90.0%; Pred. No. 1;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10

Db 246 SLFEGIDFYT 255
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Search completed: September 15, 2004, 10:35:44 Job time : 36.3158 secs

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Sequence 33352, A Sequence 12954, A Sequence 12954, A Sequence 12954, A Sequence 8613, Ap Sequence 8613, Ap Sequence 8611, Ap Sequence 2016, Ap Sequence 2016, Ap Sequence 220, App Sequence 22, App Sequence 62, 
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52, Appl
53, Appl
54, Appl
55, Appl
497, Appl
27, Appl
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29.609 Million cell updates/sec
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

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5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-60-855-632-123

US-60-879-062-12954

US-60-579-062-12954

US-60-579-062-8613

US-60-579-062-8613

US-60-579-062-8611

US-60-581-351-2016

US-60-579-062-8611

US-60-591-351-2016

US-10-501-351-351-351

US-60-5949-0032-2409

US-10-301-331-1219

US-10-301-331-1219

US-10-301-324-1219

US-10-301-324-1219

US-10-36-425-621

US-60-56-425-625

US-60-56-425-625

US-60-56-425-625

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US-60-570-505-53

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                                                                                                                                                                                                                                                                                                                                    725134 seqs, 134019282 residues
                                                                                                              September 15, 2004, 10:34:32
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Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seg length: 200000000
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Maximum DB
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Sequence 28, Appl Sequence 29, Appl Sequence 30, Appl Sequence 403, Appl Sequence 655, Appl Sequence 657, Appl Sequence 657, Appl Sequence 41, Appl Sequence 43, Appl Sequence 14, Appl Sequence 14, Appl Sequence 10, Appl Sequence 2015, Appl Sequence 2026, Appl Sequen		Other Molecules Associated With or Plant Improvement	Length 181; ; Indels 0; Gaps 0;	Shock o A Discrete Domain and is
US-60-576-801-28 US-60-576-801-29 US-60-576-801-30 US-60-576-801-30 US-60-576-812-653 US-60-576-812-655 US-60-576-812-657 US-60-592-191-41 US-60-592-191-42 US-60-592-191-43 US-60-592-191-43 US-60-592-191-43 US-60-592-191-43 US-60-592-191-43 US-60-592-191-43 US-60-592-191-43 US-60-592-191-44 US-60-592-191-44 US-60-592-191-44 US-60-592-191-44 US-60-592-191-44 US-60-592-191-44 US-60-592-191-44 US-60-592-191-44 US-60-592-191-44 US-10-451-467A-191-46 US-10-885-523-10 US-60-581-351-2015 US-60-581-351-2019 US-60-581-351-2019	ALIGNMENTS	7701 olecules and es Thereof Fc 767,701	Score 47; DB 6; Pred. No. 0.26; 0; Mismatches 1	1885-523-12 1-885-523-12 1-885-523-12 1-885-523-12 1-885-523-12 1-885-523 1-885-523-12 1-885-523
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		701-3352 s 3352, Application INFORMATION: INFORMATION: INT: Coo, Youlde, INT: Cao, Yongwei NT: Cao, Yongwei NT: Cao, Yongwei NF INVENTION: Nuclei NF INVENTION: Plant FERRENCE: 38-21(5553 FILING DATE: 2004 OF SEQ ID NOS: 6312 OF SEQ ID NOS: 6312 INFORMATION: Clone INFORMATION: Clone INFORMATION: Clone INFORMATION: Clone INFORMATION: Clone	Similarity 9 9 9; Conservati 10   SLFEGIDIXT 10   SLFEGIDENT 72   SLFEGIDENT 72	Applica MATION: uang, Q Knichen Chicken Chicken Pallise Chen, J Young, I EMPION: ENTION: ENTION: ENTION: ENTION: ENTION: ENTION: ENTION: ENTION: ALL AND
		UT 1 0-767-701-3 quence 3335 WDEAL INFORMI: PPLICANT: PPLICANT: ITLE OF INV IT	[3]	SULT 2 -10-885-523-1 500-00-12-12-31-1 500-00-00-12-31-1 500-00-00-00-00-00-00-00-00-00-00-00-00-
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 Sequence   Se	Query Ma Best Loc Matches Qy	RESULT 2 US-10-885-523-12 US-10-885-523-12 SEQUENCE 12, Application US GENERAL INFORMATION: APPLICANT: Huang, Qian APPLICANT: Richmond, Joan APPLICANT: Richmond, Joan APPLICANT: Palliser, Debo APPLICANT: Palliser, Debo APPLICANT: Palliser, Debo APPLICANT: Palliser, Debo APPLICANT: PRISEN JAMENTON: IN VIITLE OF INVENTION: IN VIITLE OF INVENTION: CD4+7; FILE REFERENCE: 0399.2006 CURRENT FILING DATE: 2006 PRIOR APPLICATION NUMBER:

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APPLICANT: Zhang, Bei TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and TITLE OF INVENTION: Compositions Thereof TITLE OF INVENTION: Compositions Thereof TITLE OF INVENTION: Compositions Thereof TITLE APPLICATION NUMBER: US/60/565,632 CURRENT APPLICATION NUMBER: 2004-04-27 NUMBER OF SEQ ID NOS: 15449 SOFTWARE: Patentin version 3.2 SEQ ID NO 8613 I.MACHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Excess, Thomas J
APPLICANT: Larosa, Thomas J
APPLICANT: Larosa, Thomas J
APPLICANT: Nunyikwa, Tichifa R. I.
APPLICANT: We, Wei
APPLICANT: Zhang, Bei
TITLE OF INVENTION: Compositions thereof
FILE REPERBNCE: 38-21 (53403) C
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOX: 41445
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Pred. No. 0.38;
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CURRENT APPLICATION NUMBER: US/60/579,062
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8613, Application US/60565632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Monsanto Technology, LLC
APPLICANT: Baum, James A
APPLICANT: Kovalic, David K.
APPLICANT: Larosa, Thomas J.
APPLICANT: Lu, Maolong
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K.
APPLICANT: Roberts, James K.
                 CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: Patentin version 3.2
SEQ ID NO 12954
LENGTH: 263
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, ORGANISM: Diabrotica virgifera
US-60-579-062-12954
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90.0%;
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Best Local Similarity 90.0.
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Best Local Similarity 90.0.
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TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions Thereof
FILE REFERENCE: 38-21 (53403)B
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 12449
SOFTWARE: Patentin version 3.2
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0.38;
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Pred. No. 0.3;
0; Mismatches
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US-10-885-523-12
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   PRIOR APPLICATION NUMBER: PCT/US00/32831
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 209
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Pred. No.
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18-60-579-062-12954

1 Sequence 12954, Application US/60579062

1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12954, Application US/60565632 GENERAL INFORMATION: APPLICANT: Monsanto Technology, LLC
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Munyikwa, Tichifa R. I.
Roberts, James K.
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APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maclong
APPLICANT: Mnnyikwa, Tichifa R.
APPLICANT: Roberts, James K
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Kovalic, David K.
Larosa, Thomas J.
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                           TYPE: PRT
ORGANISM: Unknown
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APPLICANT: CANT: CANT: CANTED TO TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and TITLE OF INVENTION: Compositions thereof TITLE OF INVENTION: Compositions thereof TITLE REPERBNICE: 38-21 (53403) C CURRENT APPLICATION NUMBER: US/60/579,062 CURRENT FILING DATE: 2004-06-11 NUMBER OF SEQ ID NOS: 41445 SOFTWARE: Patentin version 3.2 SEQ ID NO 8611 LENGTH: 639
                                                                                                                              0;
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Sequence 2016, Application US/60581351

Sequence 2016, Application US/60581351

GENERAL INFORMATION:

APPLICANT: Laurie, Cathy C

TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants

TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants

TITLE OF INVENTION: 00-10-17

FILE REFERENCE: 30-16-37-19

CURRENT APPLICATION NUMBER: US 60/479,962

PRIOR FILING DATE: 2003-06-19

NUMBER OF SEQ ID NOS: 13980

SEQ ID NO 2016

LENGTH: 639
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         ; LOCATION: (69)...(69); OTHER INFORMATION: Xaa can be any naturally occurring amino acid US-60-565-632-8611
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OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
APPLICANT: Wu, Wei
APPLICANT: Zhann
                                                                                                                                                                                                                                                                                      ; Sequence 8611, Application US/60579062; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Baum, James A
APPLICANT: Kovallc, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maolong
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                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
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GRNERAL INFORMATION:
APPLICAMY: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REFERENCE: 38-21(53372)B
CURRENT FILIAN DATE: 2004-06-17
CURRENT PILIAN DATE: 2005-06-19
PRIOR APPLICATION NUMBER: US 60/479,962
PRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2025
LENGTH: 503
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OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
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Pred. No. 0.55;
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Pred. No. 0.74;
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Kovalic, David K.

Larosa, Thomas J.

Lu, Maolong

Munyikwa, Tichifa R. I.

Roberts, James K.
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                                  ; TYPE: PRT
; ORGANISM: Diabrotica virgifera
US-60-579-062-8613
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                                                                                                               92.2%;
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                                                                                                                              Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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US-60-565-632-8611
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SEQ ID NO 8613
LENGTH: 376
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APPLICANT: ADAMS, Mark
APPLICANT: ADAMS, MARK
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPERENCE: CLOOL381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BORNEY, SARAH C.
APPLICANT: BORNEY, SARAH C.
APPLICANT: BRISDELL, HUNTS
APPLICANT: CLARK, HILLARY
APPLICANT: APPLICANT: JACKMAN, JANET
APPLICANT: JACKMAN, JANET
APPLICANT: WILLIANG, P. MICKEY
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WOOD SET STATES OF INVENTION: Related Diseases
TITLE OF INVENTION: Related Diseases
TITLE OF INVENTION: Related Diseases
TITLE OF INVENTION: NUMBER: US/10/370,715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 22
LENGTH: 641
                                    APPLICANT: Andarmani, Suean APPLICANT: Andarmani, Suean APPLICANT: Tang, Y. Tom TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia FILE REPRENCE: 821A CURRENT APPLICATION NUMBER: US/10/821,234 CURRENT APPLICATION NUMBER: US/0/82,047 PRIOR APPLICATION NUMBER: US 60/462,047 PRIOR PILING DATE: 2003-04-07 NUMBER OF SEQ ID NOS: 1704 SOFTWARE: pt SEQ_Genes Version 1.0 SEQ ID NO 1519 LENGTH: 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-370-715B-22
Sequence 22, Application US/10370715B
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-821-234-1519
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Best Local Similarity
Matches 9; Conserve
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US-10-170-205E-32659
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GENERAL INFORMATION:
APPLICANT: Bristol-Wyers Squibb Company
APPLICANT: Bristol-Wyers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT FILING DATE: 2004-07-09
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SOFTWARE PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2409, Application US/09949003C
Sequence 2409, Application US/09949003C
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: DISORDERS: WOS949,003C
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,446
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 74065
SOFTMARE: Patentin version 3.2
SEQ ID NO 2409
LENGTH: 641
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                        Score 47; DB 7; Length 639;
Pred. No. 0.95;
0; Mismatches 1; Indels
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US-09-949-003C-2409
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US-10-501-035-326
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LENGTH: 640
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us-09-673-795-2.rapn

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Query Match 92.2%; Score 47; DB 6; Length 641; Best Local Similarity 90.0%; Pred. No. 0.95; Matches 9; Conservative 0; Mismatches 1; Indels
; SEQ ID NO 32659
; IENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-32659
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286 SLFEGIDFYT 295
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Search completed: September 15, 2004, 10:48:20 Job time : 45.2632 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

September 15, 2004, 10:31:26 Run on:

% 'Search time 12.6316 Seconds (without alignments) 76.152 Million cell updates/sec

US-09-673-795-2

SLFEGIDIYT 10 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		dnaK-tvpe molecula	molecul	k protei	77070	shock		type m	molecul	molecui	FILT OF CM	molecul						_									077			heat aboat aretain	
SUMMARIES		B44261	I51344	T45477	T45479	T45476	T45478	T45471	A25646	A48872	831766	JC1391	\$20139	HHKW7A	A29160	837394	T21394	T43724	853357	S35718	I54542	A45871	HHBYA1	JH0095	B36590	A45635	112	T46650	HHXL70		1
DB	1	~	7	7	7	7	N	0	0	(1	7	7	7	Н	0	0	N	ď	7	7	7	7	Н	7	7	~	N	~	Н	C	ı
Length		208	278	467	467	468	469	632	634	636	638	639	639	640	640	640	640	640	641	641	641	641	642	642	642	644	645	646	647	647	!
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dnaK-type molecula	dnaK-type molecula	dnaK-type molecula	dnaK-type molecula	heat-shock protein	heat-shock protein	dnaK-tvpe molecula	heat shock protein	dnaK-tvpe molecula	dnaK-tvpe molecula	heat shock protein	heat shock protein	dnaK-tvpe molecula	dnaK-tvpe molecula	dnaK-tvne molecula	dnak-type molecula
A44261	A03309	PQ0138	I46588	T45473	T45474	JN0668	PC7036	825585	809036	T45517	JC7132	S48024	S48025	A34041	T45468
01	~	0	7	N	N	0	N	~	N	N	N	N	N	~	N
209	214	372	379	467	467	641	641	643	643	651	651	209	209	630	636
90.2	90.2	90.2	90.2	90.2	90.2	90.2	90.2	90.2	90.2	90.2	90.2	86.3	86.3	86.3	86.3
46	46	46	46	46	46	46	46	46	46	46	46	44	44	44	44
30	31	32	33	34	35	36	37	38	99	40	41	42	43	44	45

# ALIGNMENTS

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dnax-type molecular chaperone HSC70 - California sea hare (fragment)

Nylternate names: heat shock protein 70 homolog HSC70

Species: Aplyasia californica (California sea hare)

C;Becies: Aplyasia californica (California sea hare)

C;Becies: Aplyasia californica (California sea hare)

C;Accession: B44261

S;Kuhl, D: Kemmedy, TE:, Barzillai, A.; Kandel, B.R.

J. Call Biol. 119, 1069-1076, 1992

A;Title: Long-term sensitization training in Aplysia leads to an increase in the express harden number: A44261; MUID:93077669; PMID:1360013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: B44261
A, Status: preliminary; not compared with conceptual translation
A, Wolecule type: mucleic acid
A, Residues: 1-208 «KUH»
A, Residues: 1-208 «KUH»
A, Residues: 1-208 «KUH»
A, Residues: Bequence extracted from NCBI backbone (NCBIP:118950)
C, Genetics: A, Gene
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ö 1; Indels Score 47; DB 2; Pred. No. 0.086; 0; Mismatches 1 92.2%; 9; Conservative Query Match Best Local Similarity Matches 9; Conserv

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SLFEGIDFYT 141 1 SLFEGIDIYT 10 132 g ð

### RESULT 2

diak-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)
Nylternate names: 70K heat shock protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999
C;Accession: 151344 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999
R;Kothary, R.K.; Jones, D.; Candido, B.P.M.
Mol. Cell. Biol. 4, 1785-1791, 1984
A;Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization of CA;Reference number: 151344; MUID:85036330; PMID:6092938
A;Accession: 151344
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-278 «KOT»
A;Residues: 1-278 «KOT»
A;Cross-references: GB:KO2549; NID:g213803; PIDN:AAA49562.1; PID:g213804
C;Function: involved in protein folding and assembling/disassembling of protein compl C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

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285 SLPEGIDFYT 294
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heat-shock protein 70 [imported] - Funiculina quadrangularis
c;Species: Funiculina quadrangularis
c;Species: Puniculina quadrangularis
c;Accession: T45476
R;Borchiellini, C; Le Parco, Y,
submitted to the EMBL Data Library, September 1997
A;Reference number: Z22983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hear-shock protein 70 [imported] - Eunicella cavolini (fragment)
C;Species: Eunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T454Pi
R;Borchiellini, C.; Le Parco, Y.
R;Borchiellini, C.; Le EMBL Data Library, September 1997
A;Reference number: Z22983
                                                                                                                                                                                                                           heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)
C,Species: Chondrosia reniformis
C,Date: 31-Jan_2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
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Pred. No. 0.21;
0; Mismatches 1; Indels
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              Length 278;
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                                                       1; Indels
                                                                                                                                                                                                                                                                                         C; Accession: T45477
R; Borchiellini, C.; Le Parco, Y.
R; Borchiellini, C.; Le Parco, Y.
R; Reference number: Z22983
A; Accession: T45477
A; Status: preliminary; translated from GB/EWBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-467 < BOR>
A; Cross-references: EWBL: AF026517; PIDN: AAC05362.1
C; Genetics:
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-467 < BOR>
C,Genetics:
              Score 47; DB 2;
Pred. No. 0.12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: Hsp70
C;Superfamily: heat shock protein 70
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Best Local Similarity 90.0%;
Matches 9; Conservative (
                  92.2%;
Query Match
Best Local Similarity 90.0.
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Max. Type molecular chaperone hsc70 [imported] - slime mold (Dictyostellum discoideum)
N.Alternate names: heat shock cognate protein 70
C.Species: Dictyostellum discoideum
C.Species: Dictyostellum discoideum
C.Date: 31-Jan.2000 #sequence_revision 31-Jan.2000 #text_change 18-Feb-2000
C.Accession: T45471
R.Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.
submitted to the EMBL Data Library, September 1997
A.Reference number: Z22980
A.Accession: T45471
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
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Deat-shock protein 70 [imported] - Eunicella cavolini (fragment)
C;Species: Eunicella cavolini
C;Species: Eunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45478
R;Bordhiellini, C; Le Parco, Y.
Submitted to the EMBL Data Library, September 1997
A;Reference number: Z22983
A;Accession: T45478
A;Accession: T45478
A;Accession: T45478
A;Accession: T45478
A;Colecule type: mRNA
A;Residues: 1-469 < BOR>
A;Colecule type: mRNA
A;Colecule type: m
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 468;
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A)Accession: T45476
A)Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
A;Residues: 1-468 < BCR>
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 92.2%; Score 47; DB 2; Best Local Similarity 90.0%; Pred. No. 0.21; Matches 9; Conservative 0; Mismatches
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A;Cross-references: EMBL:AF025951; PIDN:AAB81865.1
A;Experimental source: strain AX3
                                                                                                                                                                                               A,Cross-references: EMBL:AF026516; PIDN:AAC05361.1
Genetics: Hsp70
C,Superfamily: heat shock protein 70
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A;Gene: hsc70
A;Note: localized to fillopodias and cortex C;Superfamily: heat shock protein 70
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Matches 9, Conservative
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Matches 9, Conservative
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A;Description: involved in protein folding and assembling/disassembling of protein comp;
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: JC1391
R;Sconzo, G.; Scardina, G.; Ferraro, M.G.
R;Sconzo, G.; Scardina, G.; Ferraro, M.G.
A;Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70
A;Reference number: JC1391; MUID:93077053; PMID:1339375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dnaK-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)
N;Alternate names: heat shock protein 70IV; hsp70IV protein
C;Species: Paracentrotus lividus (common urchin)
C;Dacies: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
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NyAlternate names: heat shock protein YG102; protein L0971; protein YLL024c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevision
C;Accession: S20139; S64772; S64775; S69383
R;Slater, Mr.P. Traig, RA.
Nucleic Acids Res. 17, 805-806, 1989
A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.
A;Reference number: S20139; MUID:89128457; PMID:2644626
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A;Cross-references: BMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
A;Experimental source: kidney; cell line COS-1
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Pred. No. 0.3;
0; Mismatches
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A; Reference number: S31766
                           A;Accession: S31766
A;Molecule type: mRNA
A;Residues: 1-638 <SAI>
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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A,Introns: 61/2
C,Function:
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Op
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Whateranee names: 70k heat shock cognate protein aginactin; F-actin capping protein agin

C;Species: Dictyostellum discoideum

C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999

C;Accession: A48872

R;Eddy, K.J.; Sauterer, R.A.; Condeelis, J.S.

J. Biol. Chem. 268, 22267-23274, 1993

A;Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an A;Reference number: A48872; MUID:94043116; PMID:8226849
                                                                                                                  NyAlternate names: heat shock protein 70 (Species Gallus gallus (chicken) 70 (Spacession: A25646 Hsequence_revision 19-Nov-1988 #text_change 20-Aug-1999 (Spacession: A25646 Hs.) Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S. A;Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene. A;Reference number: A25646; MUID:86304452; PMID:3017985
                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-634 <MOR>
A; Residues: 1-634 <MOR>
A; Cross-references: GB:J02579; NID:G211940; PIDN:AAA48825.1; PID:G211941
A; Cross-references: GB:J02579; NID:G211940; FIDN:AAA48825.1; PID:G211941
C; Function:
C; Function:
C; Function:
C; Superfamily: heat shock protein folding and assembling/disassembling of protein compl C; Reywords: ATP; molecular chaperone
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N;Alternate names: heat shock protein 70
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Accession: S31766; 136927
C;Accession: S31766; 136927
R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
submitted to the EMBL Data Library, January 1993
A;Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mRNÅ
A,Residues: 1-636 <EDD>
A,Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
A,Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Description: involved in protein folding and assembling/disassembling of protein compl
C,Superfamily: heat shock protein 70
C,Keywords: ATP; molecular chaperone
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Pred. No. 0.3;
0; Mismatches 1; Indels
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Pred. No.
                                                               A25646
dnaK-type molecular chaperone - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Best Local Similarity

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Query Match Matches

A;Accession: A48872 A;Status: preliminary

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Best\_Local Similarity Matches 9; Conserv

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Query Match

A; Molecule type: DNA

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dnaK-type molecular chaperone HSPAIL - human
N.Alternate names: heat shock protein, 70K
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: A29160, 137561, 137562
R;Hunt, C: Morimoto, N. I.
Proc. Natl. Acad. Sci. U.S. 82, 6455-6459, 1985
A;Pitle: Conserved features of eukaryotic hsp70 genes revealed by comparison with the name on unbers A29160; MUID: 86016721, PMID: 3931075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A29160
A; Molecule type: DNA
A; Residues: 1-640 «HUN>
A; Residues: 1-640 «HUN>
A; Residues: 1-640 «HUN>
A; Residues: 1-640 «HUN>
A; Residues: Experiment of the authors mistranslated residues 463, 491, and 492
A; Note: the authors mistranslated residues 463, 491, and 492
B; Cross-references: GB: MI1717; GB: MI5432; NID: G184416; PIDN: AAA52697.1; PID: G386785
A; Note: the authors mistranslated residues 463, 491, and 492
B; Databent, B.; Genthe, A.; Benecke, B.J.
Nucleic Acids Res. 14, 8933-8948, 1986
A; Reference number: 137561; MUID: 87066768; PMID: 3786141
A; Reference number: 137561; MUID: 87066768; PMID: 3786141
A; Accession: 137561
A; Residues: translation not shown; translated from GB/EMBL/DDBJ
A; Residues: 1-22 «RBS>
A; Cross-references: EMBL: X04676; NID: G32480; PIDN: CAA28381.1; PID: G32481
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C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Distribute molecular chaperone hsc70 - slime mold (Dictyostellum discoideum)
N.Alternate names: heat shock cognate protein 70
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: 837394
R;Haus, U.; Trommler, P.; Fisher, P.R.; Hartmann, H.; Lottspeich, F.; Noegel, A.A.; Sch
EMBO J. 12, 3763-3771, 1993
A;Pitle: The heat shock cognate protein from Dictyostellum affects actin polymerization
A;Reference number: 837394; WUID:94008983; PMID:8404847
A;Accession: 837394
A;Molecule type: mRNA
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A;Molecule type: DNA
A;Residues: 616-640 <RE2>
A;Cross-references: EMBL:X04677; NID:g32482; PIDN:CAA28382.1; PID:g32483
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C;Keywords: ATP; heat shock; molecular chaperone; stress-induced
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                                                                    Length 640;
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                                                                    Score 47; DB 1;
Pred. No. 0.3;
0; Mismatches
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Pred. No. 0.3;
0; Mismatches
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A;Map position: 6p21.3 - 6p21.3
A;Introns: #status absent
G;Function:
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90.0%;
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Matches 9; Conserv
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A; Molecule type: DNA; mRNA
A; Residues: 1-40 < < SNU;
A; Rolecule type: DNA; mRNA
A; Residues: 1-40 < < SNU;
A; Note: genomic clones representing six distinct members of the hisp70 gene family were in A; Note: genomic clones representing six distinct members of the hisp70 gene family were in A; Note: one of the three introns in hsp70A is in a position similar to an intron in Dros C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Fromtion:
C; Fruction:
C; Fruction:
C; Superfamily: heat shock protein folding and assembling/disassembling of protein complicition:
C; Superfamily: heat shock protein 70
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N;Alternate names: heat shock protein 70 A
(Species: Caenorhabditis elegans
C;Beccies: Caenorhabditis elegans
C;Accession: UT0288
R;Snutch, T.R.; Heschl, M.F.P.; Baillie, D.L.
Gene 64, 241-255, 1988
A;Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characterizat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: involved in protein folding and assembling/disassembling of protein compl C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A;Residues: 1-639 <G0P-
A;Cress-references: EMEL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YLL02
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S64775
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: NA
A; Molecule type: NA
A; Molecule type: NA
A; Molecule type: SMBL: Z73129; MIPS: YLL024c
A; Molecule to the EMBL is an S288C
A; Molecule to the EMBL Data Library, April 1996
A; Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14
mily and a new ABC transporter homologous to the human multidrug resistance protein.
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A;Residues: 1-639 <PUR>
A;Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007
                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D. submitted to the Protein Sequence Database, May 1996
A;Reference number: S64775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                        A;Cross-references: EMEL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546 R;Goffeau, A.; Purnelle, B. Rigoffeau, A.; Purnelle, B. Submitted to the Protein Sequence Database, May 1996 A;Reference number: S64761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No. 0.3;
0; Mismatches 1; Indels
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Best Local Similarity 90.0%;
Matches 9; Conservative
                                                       A; Status: translation not shown
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                                                                                         A; Molecule type: DNA
A; Residues: 1-639 <SLA>
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A;Residues: 1-640 <HAU>
A;Cross-references: EMBL:X75263; NID:g433874; PIDN:CAA53039.1; PID:g433875
C;Genetics: hsc70
C;Genetics: hsc70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl C;Superfamily: heat shock protein 70
C;Reywords: AIP; molecular chaperone
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0
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Search completed: September 15, 2004, 10:36:13 Job time : 12.6316 secs

284 SLFEGIDEYT 293

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September 15, 2004, 10:34:17; Search time 312.632 Seconds (without alignments) 31.221 Million cell updates/sec
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ptodata/2/paa/US106_COMB.pep:*
ptodata/2/paa/US107_COMB.pep:*
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'ptodata/2/paa/US102_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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51
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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description ID Query Score Match Length DB No. Result

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447 W 44	1158 7 763 8 3 229, 7 763 11 11 11 11 11 11 11 11 11 11 11 11 11	124261, 12366, 12366, 12366, 10433, 10433, 18846, 10496, 10496, 10496, 18475, 26883, 2, Appl
US-09-673-795-2 US-10-110-731-2 US-10-110-731-3 US-10-110-731-3 US-10-110-731-3 US-09-417-507-224 US-09-791-537-306 US-09-791-537-596 US-09-791-537-596 US-09-791-537-636 US-09-791-537-643 US-09-791-537-643 US-09-791-537-643 US-09-791-537-643 US-09-791-537-643 US-09-791-537-643	US-10-408-7653-71586, US-10-408-7631-7631 US-60-412-31-1586, US-60-412-31-1586, US-10-328-953-319 US-10-328-953-329 US-10-328-953-329 US-10-328-953-329 US-10-328-953-329 US-09-791-537-76315 US-09-791-537-79	US-09-791-537 1242 US-10-366-9433-1236 US-09-791-537-6434 US-09-791-537-6434 US-09-935-625-3697 US-09-935-625-1043 US-09-935-625-1043 US-09-935-625-1043 US-09-935-625-1043 US-09-935-625-1043 US-09-935-625-1043 US-09-935-625-1043 US-09-935-625-1043 US-09-935-625-1043 US-09-935-625-1043
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## ALIGNMENTS

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Sequence 2, Application US/09673795
GENERAL INFORMATION:
APPLICANT: TRIBERL, FREDERIC
APPLICANT: TRIBERL, FREDERIC
TITLE OF INVENTION: MUTATED PEPTIDE COMPOUNDS, DERIVED FROM hsp70, USEFUL IN CANCER
TITLE OF INVENTION: MMUNOTHERAPY
TITLE OF INVENTION: MMUNOTHERAPY
TITLE OF INVENTION: IMMUNOTHERAPY
TITLE OF INVENTION: IMMUNOTHERAPY
FILE REPRENENCE: 03155.0069
CURRENT APPLICATION NUMBER: US/09/673,795
CURRENT FILING DATE: 1999-04-22
FRIOR APPLICATION NUMBER: FF 98 05033
FRIOR APPLICATION NUMBER: FF 98 05033
FRIOR APPLICATION NUMBER: FF 98 05033
FRIOR FILING DATE: 1998-04-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Vers. 2.1
SEQ ID NO 2
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT;
CORGANISM: Homo sapiens
US-09-673-795-2
US-09-673-795-2
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1 SLFEGIDIYT 10
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                                                                                                                                                                                                                                                                                                                                                                                                           1 SLFEGIDFYT 10
                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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ORGANISM: Glycine max
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APPLICANT: TRIBBEL, REDERIC
APPLICANT: GAUDIN, CATHERINE
TITLE OF INVENTION: MUTATED PEPTIDE COMPOUNDS, DERIVED FROM hsp70, USBFUL IN CANCER
TITLE OF INVENTION: IMMUNOTHERAPY
FILLE REFERENCE: 03715.0069
CURRENT APPLICATION NUMBER: US/09/673,795
CURRENT APPLICATION NUMBER: PCT/FR99/00957
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1998-04-22
PRIOR FILING DATE: 1998-04-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VOIS: 2.1
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TITLE OF INVENTION: NEW LYMPHOCYTES, A PROCESS FOR PREPARING THE SAME AND
TITLE OF INVENTION: THEIR USE IN THERAPEUTICS
FILE REFREENCE: WOB 99 BA IDM STRE
CURRENT APPLICATION NUMBER: US/10/110,731
PRIOR APPLICATION NUMBER: EP 99 120 484.3
PRIOR FILING DATE: 1999-10-15
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Query Match 100.0%; Score 51; DB 20; Length 10; Best Local Similarity 100.0%; Pred. No. 0.0094; Matches 10; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.058;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 10
TYPE: PRT
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Best Local Similarity 100.
Matches 10; Conservative
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CORGANISM: Homo sapiens
US-09-673-795-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-110-731-2
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Best Local Similarity
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US-10-110-731-3
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-10-110-731-2
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APPLICANT: La Rosa Thomas J
APPLICANT: Ea Rosa Thomas J
APPLICANT: Evolutic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 255293
LENGTH: 174
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APPLICANT: KEITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: FUMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-10
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 22471
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APPLICANT: I.D.M. IMMUNO-DESIGNED MOLECULES
TITLE OF INVENTION: NEW LYMPHOCYTES, A PROCESS FOR PREPARING THE SAME AND
TITLE OF INVENTION: THEIR UGE IN THERAPEUTICS
FILE REFERENCE: WOB 99 BA IDM STRE
CURRENT APPLICATION NUMBER: US/10/110,731
CURRENT FILING DATE: 2002-04-15 DRIOR APPLICATION NUMBER: EP 99 120 484.3
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENT VERSION 3.1
SEQ ID NO 3
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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US-10-424-599-255293
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Pred. No. 1.4;
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Pred. No. 0.058;
0; Mismatches
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LOCATION: (1)..(174)
OTHER INFORMATION: unsure at all Xaa locations
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US-10-424-599-255293
; Sequence 255293, Application US/10424599
; GENERAL INFORMATION:
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; Sequence 22471, Application US/09417507
; GENERAL INFORMATION:
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90.0%;
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Best Local Similarity 90.v.
...a 9; Conservative
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Sequence 5964, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Decek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT PAPLICATION UNBER: US/09/791,537
CURRENT PALING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE PALENT VERSION 3.0
SEQ ID NO 5964
LENGTH: 220
                                                                                                                                                                                                                                                                                       APPLICANT: BORAZZI, Vivien
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPREBUCE: CLOO0451
CURRENT APPLICATION NUMBER: US/60/196,712
CURRENT APPLICATION NUMBER: 2000-04-13
NUMBER OF SEQ ID NOS: 3846
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 212
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                                    DB 22; Length 209;
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                                                  Pred. No. 1.7;
0; Mismatches
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                                    Score 47;
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US-09-791-537-120833
; Sequence 120833, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
                                                                                                                                                                                                                                US-60-196-712-2253; Application US/60196712; GENERAL INFORMATION:
                             92.2%;
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US-09-791-537-5964
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                         Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                              SLFEGIDIYT 10
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Best Local Similarity
Matches 9; Conserv
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; ORGANISM: HUMAN
US-60-196-712-2253
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APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: HEREE DIMMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261,210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 3064
LENGTH: 208
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Sequence 12. Application US/09761534A

SERVICANT: Huang, Qian

APPLICANT: Richmond, Joan F.L.

APPLICANT: Chen, Bryan K.

APPLICANT: Chen, Janzhu

APPLICANT: Chen, Janzhu

APPLICANT: Chen, Wichard A.

TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock

TITLE OF INVENTION: Debter Fusion Proteins Maps To A Discrete Domain and is

TITLE OF INVENTION: DA+T Cell-Independent

FILE REFREENCE: 0399_2006_003

TITLE OF INVENTION: DA+T Cell-Independent

FILE REFREENCE: 0399_2006_003

CURRENT APPLICATION NUMBER: US/09/761,534A

CURRENT FILING DATE: 2000_01_16

PRIOR FILING DATE: 2000_01_16

PRIOR FILING DATE: 2000_01_14

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12

TAPR: DATE: 209

TAPR: DATE: 209
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                                                                                                 Score 47; DB 18; Length 175;
Pred. No. 1.4;
0; Mismatches 1; Indels
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Pred. No. 1.7;
0; Mismatches 1;
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OTHER INFORMATION: Murine hsp70 - Segment II
US-09-761-534A-12
                                                                                                                                                                                                                                                                                                                       Sequence 3064, Application US/09791537 GENERAL INFORMATION:
                                                                                                 92.2%;
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Aplysia californica
US-09-791-537-3064
                                                                                             Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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                ; TYPE: PRT
; ORGANISM: A.fumigatus
US-09-417-507-22471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                -09-791-537-3064
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US-09-761-534A-12
LENGTH: 175
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Gegreence 115866, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomia, Inc.
APPLICANT: Bionomia, Inc.
APPLICANT: Dancer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEWE
FILE REPRENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 133055
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank GI:15277246; amino acids 5-381 of hsp70
DATABASE ENTRY DATE: 2001-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 377
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                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 2
Pred. No. 3.4;
0; Mismatches
Pred. No. 3.3;
                         Mismatches
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90.06;
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Best Local Similarity 90.0
Matches 9; Conservative
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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US-09-791-537-115866
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US-09-791-537-115866
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LENGTH: 380
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US-10-328-953-1
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Sequence 435, Application US/09791537

Sequence 435, Application US/09791537

Sequence 435

Sequence 435, Application US/09791537

Sequence 435

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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT PAPLICATION NUMBER: US/09/791,537
CURRENT PLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 49619
        APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATCHIN VERSION 3.0
SEQ ID NO 120833
LENGTH: 278
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Pred. No. 2.4;
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Pred. No. 2.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Onchocerca volvulus
US-09-791-537-49619
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
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US-09-791-537-49619
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Wed Sep 15 10:57:57 2004

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Search completed: September 15, 2004, 10:46:48 Job time : 312.632 secs

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September 15, 2004, 10:35:52; Search time 90 Seconds (without alignments) 35.632 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/DEN_TOWN PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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51
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Semience 255293	Semience 33350 A	Semience 12. Appl	Semiance 1 April	7,7	210,7	ָ קר קר	200	Seguence 327, App	0 0	,,	,000	Sequence 3466, Ap				Sequence 22298, A
		ID	US-10-424-599-255293	US-10-767-701-33352	US-09-761-534A-12	US-10-328-953-1	US-10-408-765A-763	US-10-328-953-319	US-10-328-953-326	US-10-328-953-327	US-10-328-953-328	118-10-328-953-329	TS-10-328-953-330	20 10 10 10 10 10 10 10 10 10 10 10 10 10	US-10-108-260A-3466	US-10-369-493-12366	US-10-132-556A-2	770 70 70 70 71	US-IU-369-493-22298
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		Match Length DB	174	181	209	377	380	381	392	393	393	393	4 7 7 7		4 / 6	516	622	000	600
0/0	Query	Match	92.2	92.2	92.2	92.2	92.2	92.2	92.2	92.2	92.2	92.2	92.2		7.76	92.2	92.2	000	74.4
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Seguence 6233. Ap	Sequence 255. App	Segmence 3. Appli	Sequence 1, Appli	Sequence 146. App	Sequence 5, Appli	Sequence 28. Appl	Seguence 97, Appl	Seguence 10. Appl	a)		Sequence 146, App	2277		117	11	204	396	~	724	4304	Sequence 43012, A	Sequence 54413, A	3 12	-	equence 47010.		353	73. At	7
L5 US-10-369-493-6233	US-1	US-09-759-010-3	3-09-935-64	US-09-919-0	12 US-10-380-408A-5		14 US-10-316-253-97	US-09-761-534A-10	15 US-10-369-493-1394	15 US-10-369-493-1760		.5 US-10-369-493-22772	US-10-369-4		.0 US-09-733-179A-11		.6 US-10-755-889-396	US-09-925-302-724	.2 US-09-925-302-724		.2 US-10-425-114-43012	US-10	.6 US-10-408-765A-1256	US-10		0-320	US-10		.2 US-10-380-408A-7
640 1	640 1	641 9	641 1	641 1	641 1	641 1	641 1	642 9	642 1	642 1	642 1	650 1	761 1	9	643 1	643 1	643 1	665 9	665 1	134 1	365 1	461 1	493 1	586 1	608 1	611 1	621 1	641 1	641 1
47 92.2	47 92.2	47 92.2	47 92.2	47 92.2	47 92.2	47 92.2	47 92.2	47 92.2		47 92.2	47 92.2	47 92.2	47 92.2		46 90.2					44 86.3			ω	44 86.3	ω	44 86.3	44 86.3	44 86.3	44 86.3
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 US-10-424-599-255293

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Sequence 255233, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Last a strong solution of the control of the 
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LOCATION: (1)..(174)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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RESULT 2 US-10-767-701-33352

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wieland, Felix
APPLICANT: Wieland, Felix
TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
FILE REPRERENCE: 11390/46101
CURRENT APPLICATION NUMBER: US 1010/328,953
CURRENT FILING DATE: 2002-12-23
FRIOR PEPLICATION NUMBER: US 60/342,570
PRIOR PELING DATE: 2001-12-26
PRIOR PELING DATE: 2001-12-26
PRIOR PELING DATE: 2002-04-12
PRIOR PELING DATE: 2002-07-29
PRIOR PELING DATE: 2002-07-29
PRIOR PELING DATE: 2002-07-29
PRIOR PELING DATE: 2002-09-28
NUMBER OF SEQ ID NOS: 331
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 1
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank GI:15277246; amino acids 5-381 of hsp70
DATABASE BUTRY DATE: 2001-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FATY, BOIN D.
APPLICANT: Zhang, Bing
APPLICANT: Glason, Bradford W.
APPLICANT: Glason, Bradford W.
APPLICANT: Glason, Gary W.
APPLICANT: Glason, Cary W.
APPLICANT: Marnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICANTON NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTMARE FASLSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 90.0
Matches 9; Conservative
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Matches 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-10-408-765A-763
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Sequence 12, Application US/09761534A

Patent No. US20020144426A1

GENERAL INFORMATION:

APPLICANT: Richmond, Joan F.L.

APPLICANT: Rolliser, Deborah

APPLICANT: Chen, Jianzhu

ANUMBER OF SEQ ID NOS: 25

AVENCE: APPLICANT: Chen, Jianzhu

AVENCE: APPLICANT: Chen, Jianzhu

AVENCE: APPLICANT: Chen, Jianzhu

AVENCE: APPLICANT: Chen, Jianzhu

ANUMBER OF SEQ ID NOS: 25

AVENCE: APPLICANT: Chen, Jianzhu

                                                                                                                                     APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Mucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 33552
LENGTH: 181
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Pred. No. 0.43;
0; Mismatches 1; Indels
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US-10-767-701-33352
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US-09-761-534A-12
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                       Sequence 33352, Application US/10767701
Publication No. US20040172684A1
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US-10-328-953-1
; Sequence 1, Application US/10328953
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                                                                                   GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Sorghum bicolor
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Best Local Similarity
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US-09-761-534A-12
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; OTHER INFORMATION: fusion polypeptide: gp100(209-217:Met210)-Gly-Ser-Gly-hsp70(1-38 US-10-328-953-327
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hartl, Frana-Ulrich
TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
FILE REFERENCE: 11390/46101
CURRENT APPLICATION NUMBER: US/10/328,953
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 60/342,570
PRIOR FILING DATE: 2001-12-26
PRIOR PLING DATE: 2001-12-26
PRIOR PLING DATE: 2001-12-28
PRIOR FILING DATE: 2002-04-12
PRIOR PLING DATE: 2002-04-14
PRIOR PLING DATE: 2002-04-14
PRIOR PLING DATE: 2002-04-14
PRIOR PLING DATE: 2002-04-14
PRIOR PLING DATE: 2002-09-28
PRIOR PLING DATE: 2002-09-28
PRIOR PLING DATE: 2002-09-28
PRIOR APPLICATION NUMBER: US 60/414,834
PRIOR PLING DATE: 2002-09-28
PRIOR PLING DATE: 2002-09-28
PRIOR PLING DATE: 2002-09-28
PRIOR PLING DATE: 2003-09-28
PRIOR DATE: 2003-09-28
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Publication No. US20040071656A1

GENERAL INFORMATION:
APPLICANT: Wieland, Felix
APPLICANT: Wieland, Felix
TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
FILE REFERENCE: 11390/46401
CURRENT FILING DATE: 2002-12-23
FRIOR APPLICATION NUMBER: US 60/342,570
FRIOR APPLICATION NUMBER: US 60/342,570
FRIOR PELING DATE: 2001-12-26
FRIOR APPLICATION NUMBER: US 60/342,570
FRIOR FILING DATE: 2001-12-26
FRIOR APPLICATION NUMBER: US 60/342,570
FRIOR FILING DATE: 2002-04-12
FRIOR FILING DATE: 2002-04-12
FRIOR FILING DATE: 2002-04-29
FRIOR FILING DATE: 2002-07-29
FRIOR FILING DATE: 2002-07-29
FRIOR FILING DATE: 2002-07-29
FRIOR FILING DATE: 2002-07-39
FRIOR FILING DATE: 2003-07-39
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       Indels
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       Mismatches
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Publication No. US20040071656A1
GENERAL INFORMATION:
APPLICANT: Wieland, Felix
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ORGANISM: Artificial Sequence
9; Conservative
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Best Local Similarity
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; OTHER INFORMATION: fusion polypeptide: hsp70(1-381)-Gly-Ser-Gly-gp100(209-217:Met210
US-10-328-953-326
Sequence 319, Application US/10328953

Publication No. US20040071656A1

GENERAL INFORMATION:

APPLICANT: Wieland, Felix

APPLICANT: Hartl, Franz-Ulrich

TITE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies

FILE REFERENCE: 11390/46101

CURRENT APPLICATION WOMBER: US/10/328,953

FRIOR FILING DATE: 2001-12-26

PRIOR PLILING DATE: 2001-12-26

PRIOR FILING DATE: 2001-12-26

PRIOR FILING DATE: 2001-12-26

PRIOR FILING DATE: 2001-12-26

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-07-29

PRIOR FILING DATE: 2002-07-39

PRIOR FILING DATE: 2002-07-39

PRIOR FILING DATE: 2002-07-39

PRIOR FILING DATE: 2002-07-39

PRIOR FILING DATE: 2002-07-39
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| Sequence 326, Application US/10328953
| Publication No. US20040071656Al
| GENERAL INFORMATION:
| APPLICANT: Wieland, Felix
| APPLICANTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
| FILE REPERBYCE: 11390/46101
| CURRENT APPLICATION NUMBER: US/10/328,953
| CURRENT PILING DATE: 2002-12-23
| PRIOR PILING DATE: 2001-12-26
| PRIOR PILING DATE: 2001-12-28
| PRIOR PILING DATE: 2001-04-12
| PRIOR PILING DATE: 2002-04-12
| PRIOR PILING DATE: 2002-04-12
| PRIOR PILING DATE: 2002-04-12
| PRIOR FILING DATE: 2002-04-12
| PRIOR FILING DATE: 2002-04-13
| PRIOR FILING DATE: 2002-03-28
| NUMBER OF SEQ ID NOS: 331
| SOFTWARE: WordPerfect 8.0 for Windows
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PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: GenBank GI:15277246; amino acids 1-381 of hsp70

DATABASE ENTRY DATE: 2001-08-22

US-10-328-953-319
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Pred. No. 0.85;
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Pred. No. 0.87;
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ORGANISM: Artificial Sequence
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Best Local Similarity 90.0
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Best Local Similarity
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LENGTH: 392
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US-10-369-493-12366
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US-10-108-260A-3466
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; OTHER INFORMATION: tyrosinase(368-376;Asp370)-Gly-Ser-Gly-hsp70(1-381)
US-10-328-953-329
                              PRACTURE:
OTHER INFORMATION: fusion polypeptide:
OTHER INFORMATION: hsp70(1-381)-Gly-Ser-Gly-tyrosinase(368-376:Asp370)
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Pred. No. 0.88;
                                                                                                                                                                                                                           Score 47; DB 12; Length 393;
Pred. No. 0.88;
0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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Matches 9; Conservative
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Sequence 1236, Application US/10369493
; Sequence 1236, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Glater, Steven C.
; APPLICANT: Gloman, Barry S.
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED
; TITLE OF INVENTION: UNMER: 105/10/369,493
; CURRENT PILLING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR PILLING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12366
; LENGTH: 516
                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: fusion polypeptide: hsp70(1-381)-Gly-Ser-Gly-
; OTHER INFORMATION: gp100(209-217:Met210)-Gly-Ser-Gly-tyrosinase(368-376:Asp370)
US-10-328-953-330
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; Publication No. US20040005560A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; TILE REFERENCE: H1-A0106
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3466
; LENGTH: 476
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 405;
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90.0%; Pred. No. 0.91;
iive 0; Mismatches 1;
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PRIOR APPLICATION NUMBER: US 60/399,342
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/414,834
PRIOR FILING DATE: 2002-09-28
NUMBER OF SEQ ID NOS: 331
SOFWARR: WordPerfect 8.0 for Windows
SEQ ID NO 330
LENGTH: 405
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                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
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Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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ORGANISM: Homo sapiens
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US-10-369-493-22298
i Sequence 22284 Application US/10369493
i Sequence 22284 Application No. US20030233675A1
i GENERAL INFORMATION:
i APPLICANT: Goo, Yongwei
i APPLICANT: Hinkle, Gregory J.
i APPLICANT: Glodiman, Barry S.
i TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
i TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
i TITLE OF INVENTION: UNMERR: US/10/369,493
i CURRENT APPLICATION NUMBER: US 60/360,039
i PRIOR FILING DATE: 2002-02-21
i SEQ ID NOS: 47374
i ERGTH: 639
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                                                                                                                                                                                                                                                                     Sequence 2, Application US/1013556A
Fublication No. US20030082629A1
GENERAL INFORMATION:
APPLICANT: Volloch, Vladimir
APPLICANT: Sherman, Michael
ITILE OF INVENTION: IN THE REGILATION OF CELL PROLIFERATION
FILE REFERENCE: A32367-FCT-USA-A 066290.0106
CURRENT APPLICATION NUMBER: US/10/132,556A
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 09/936,879
PRIOR APPLICATION NUMBER: PCT/US00/07350
PRIOR APPLICATION NUMBER: PCT/US00/07350
PRIOR PRILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FEASESEQ for Windows Version 4.0
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                                          92.2%; Score 47; DB 15; Length 516; 90.0%; Pred. No. 1.2; tive 0; Mismatches 1; Indels
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Pred. No. 1.5;
0; Mismatches 1; Indels
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                                        Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                             1 SLFEGIDIYT 10
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ORGANISM: Homo sapien
US-10-369-493-12366
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                                                                                                                                                                                                                                   RESULT 14
US-10-132-556A-2
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LENGTH: 622
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283 SLFEGIDFYT 292
1 SLFEGIDIYT 10
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Search completed: September 15, 2004, 10:51:17 Job time : 90 secs

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Sequence 7125, Appliageduence 14, Appliageduence 174, Appliageduence 174, Appliageduence 174, Appliageduence 19, Appliageduence 5812, Appliageduence 5812, Appliageduence 72, Appliagedu
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107, App
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                                                                                                                                             September 15, 2004, 10:32:27; Search time 15.7895 Seconds (without alignments) 32.696 Million cell updates/sec
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(Sgn2_6/ptodata/2/iaa/6A_COMB.pep:*
(Sgn2_6/ptodata/2/iaa/6A_COMB.pep:*
(Sgn2_6/ptodata/2/iaa/6B_COMB.pep:*
(Sgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
(Sgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
(Sgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-08-797-358B-3
US-08-141-139-14
US-09-131-783A-174
US-09-107-532A-6410
US-08-487-890A-19
US-08-487-890A-19
US-08-478-373-19
US-08-474-671-19
US-08-474-671-19
US-08-474-671-19
US-08-474-671-19
US-08-483-19
US-08-483-19
US-08-483-19
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US-08-483-19
US-08-637-654-19
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US-08-478-373-107
US-08-474-671-107
US-08-893-577A-107
US-08-897-438-107
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US-08-487-890A-107
US-08-478-435-107
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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No.
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Sequence 107, App Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 8, Appli Sequence 8, Appli Sequence 52, Appli	and David Bush AND AMINO ACID SEQUENCES RELATING TO FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS CS CORPORATION 7,532A 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
911 4 US-08-649-518-107 913 1 US-08-487-890A-5 913 2 US-08-478-435-5 913 2 US-08-478-433-5 913 2 US-08-478-671-5 913 3 US-08-474-671-5 913 3 US-08-474-671-5 913 4 US-08-697-654-5 163 4 US-08-637-7638-6 332 2 US-08-637-7638-6 332 3 US-08-637-7638-8 332 3 US-08-637-7638-8 332 3 US-08-637-7638-8 332 3 US-08-637-7638-8 333 3 US-09-170-354-8 339 4 US-09-338-692-52	ALIGNW  ('09107532A  ('09107532A  CLETC ACID  TERROCOCCUS  310  (THERAPEUTI  r Street  tts  ('THERAPEUTI  r Street  tts  ('THERAPEUTI  r Street  tts  ('THERAPEUTI  r Street  tts  ('THERAPEUTI  r Street  TAS  OM ISO9660  cUnknown> TAS  CHOWNS  TAS  TAS  TAS  TAS  TAS  TAS  WHOSER: GTC  RMATION: 93-5007  83-77  7125: CS: acids  acids  ature  ATION 12  SEQ ID NO:
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 1  US-09-107-532A-7125  Sequence 7125, Application US/091  Patent No. 658375  GENERAL INFORMATION:  TITLE OF INVENTION: NUCLEI  NUMBER OF SEQUENCES: 7310  CORRESPONDENCE ADDRESS: 7310  CORRESPONDENCE ADDRESS: 7310  CORPUTER: Massachusetts  CUNTRY: USA  ZIP: 02354  COMPUTER: PCCOMPUTER: PCCOMPUTER: PCCOMPUTER: PCD/ROM I  COMPUTER: PCCOMPUTER: PCC
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1 US-09-107- 1 Sequence 1 Patent N 1 GENERA 1

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; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSC70
US-09-513-783A-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.3%; Score 44; DB 1; Length 646; 80.0%; Pred. No. 1.9;
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US-09-513-783A-174
US-09-513-783A-174

j Sequence 174. Application US/09513783A
j Patent No. 6416959
j GENERAL INFORMATION:
j APPLICANT: Giuliano, Kenneth A.;
j APPLICANT: Kapur, Ravi
j TITLE OF INVENTION: A System for Cell Based Screening;
j TITLE OF INVENTION: A System for Cell Based Screening;
j CURRENT APPLICATION NUMBER: US/09/513,783A
j CURRENT APPLICATION NUMBER: US/09/513,783A
j CURRENT FILING DATE: 2000-02-25
j NUMBER OF SEQ ID NOS: 180
j SSEQ ID NO 174
j LENGTH: 890
                            ADDRESSER: SCULIY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City Plaza CITY: Garden City Plaza CITY: Garden City Plaza CITY: Garden City Plaza COUNTRY: USA ZIP: 11530 COMPUTER: BADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Par PROPERATION PATA: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/089,997 FILING DATE: 15-MAY-1995 CLASSIFICATION NUMBER: US 08/089,997 FILING DATE: O6-JUL-1993 PRICH APPLICATION NUMBER: US 08/089,997 FILING DATE: NAME: DIGIGILO: Frank S. REGISTRATION: NUMBER: 31,346 FEBRESTERATION NUMBER: 31,346 FEBRESTERATION: NUMBER: 31,346 FEBRESTERATION: NUMBER: 31,346 FEBRESTERATION NUMBER: 31,346 FEBRESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEY: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 646 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 86.3
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:|||| ||
286 SLYEGIDFYT 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SLFEGIDIYT 10
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CORRESPONDENCE ADDRESS:
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                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08797358B
Sequence 3, Application US/08797358B
Patent No. 6268478
GENERAL INFORMATION:
APPLICANT: Adams, John
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Johla Village Drive, Suite 700
CITY: San Diego
STRTE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION NUMBER: US 60/011,491
FILING DATE: 12-FEB-1996
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 3; Length 643;
Pred. No. 0.8;
1; Mismatches 1; Indels
                                                     Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
NUMBER OF SEQUENCES: 20
                                                                                                                                    0; Indels
                                                     DB 4;
                                                     Score 46; DB 4;
Pred. No. 0.26;
1; Mismatches
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STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-441-139-14
Sequence 14, Application US/08441139
; Patent No. 5773245
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                                                     90.2%;
                    Query Match
Best Local Similarity 88.5.
8, Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                 189 LFEGIDVYT 197
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US-08-797-358B-3
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66.7%; Score 34; DB 1; Length 36;

Best Local Similarity 75.0%; Pred. No. 6.9;

Matches 6; Conservative 1; Mismatches 1; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Batentin Release #1.0, Version #1.25
SUSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-UN-1993
CLASSIFICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
APPLICATION NUMBER: US 08/148,968
FILING DATE: (10-NOV-159)
APPLICATION NUMBER: US 08/148,968
ATTORNEY PROPERTION NUMBER: US 08/148,968
APPLICATION NUMBER: US 08/148,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               68.6%; Score 35; DB 4; 75.0%; Pred. No. 48; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Sim & McBurney
6th Floor, 330 Unviersity Avenue
                                                                                                            NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...319; SEQUENCE DESCRIPTION: SEQ ID NO: 6410:US-09-107-532A-6410
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/08487890A
Patent No. 5708149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jacenc No. J. J. J. GENERAL INFORMATION:
APPLICANT: LOOSMOYE, Sheena
APPLICANT: Harkness, Robin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 amino acids
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||:||||:
126 LFQGIDIF 133
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Patent No.
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                      Sequence 532, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILIAG DATE: 1998-08-13
FILE REPERBYCE: 032796-032
CURRENT FILIAG DATE: 1998-08-13
FRIOR PELING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTI VETSION 3.1
SEQ ID NO 5332
LIENGTH: 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELERPONE: (781)893-6007
TELERPAX: (781)893-8077
INFORMATION FOR SEQ ID NO: 6410:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6410, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Enterococcus faecalis
US-09-134-000C-5332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|:||::|
28 SIFDGIEVY 36
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              RESULT 5
US-09-134-000C-5332
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US-09-107-532A-6410
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Gaps

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ADDRESSES: _____
STREET: Suite 701, 330 Unviersity Avenue
CITY: Toronto
CITY: Toronto
CITY: Canada
COUNTRY: Canada
ZIP: MSG IR7
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
COMPUTER: PLODS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION (415
ATTORNEY/ARENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCY DOCKET NUMBER: 1038-410 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMU
                                                                                               APPLICANT: Harkness, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Harkness, Robin
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Wang, Yan-Ping
APPLICANT: Wang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Sille 701, 330 Unviersity Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/08478373
Patent No. 5922841
GENERAL INFORMATION:
Sequence 19, Application US/08337483 Patent No. 5922562 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 FEGIDIYT 10
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                                                                                                                                                                                                                                                                                          US=-US=-4.8-4.5-1.9

Sequence 19, Application US/08478435

Sequence 19, Application US/08478435

Sequence 19, Application US/08478435

Sequence 19, Application US/08478435

Septent No. 592233

Septent No. 592223

APPLICANT: Locomore, Sheena APPLICANT: Chong, Pele APPLICANT: Chong, Pele APPLICANT: Murdin, Andrew APPLICANT: Wilein, Michel TITLE OF INVENTION: Transferrin Receptor Genes APPLICANT: Wilein, Andrew APPLICANT: Wilein, Michel TITLE OF INVENTION: Transferrin Receptor Genes CITY: Toronto STREET: Suite 701, 330 University Avenue CITY: Toronto CONRESSEE: Sim & McBurney STREET: Suite 701, 330 University Avenue CITY: Toronto CONFUTEN: ENAPABLE FORM:

MEDIUM TYPE: Floopy disk Compatible CONFUTEN: Toronto CONFUTEN: DATE-CONFUTEN: PC-DOS/MS-DOS SOTTWARE: PREPLICATION DATA: APPLICATION NAME: US/08/478,435

COMPUTEN: OBSETE: 07-UTW-1995

COMPUTEN: OBSETE: 07-UTW-1995

COMPUTEN: OBSETE: 07-UTW-1995

CLASSIFICATION NUMBER: US 08/175,116

FILING DATE: 08-NOV-1993

APPLICATION NUMBER: US 08/148,968

FILING DATE: 08-NOV-1993

APPLICATION NUMBER: US 08/175,116

FILING DATE: 08-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 amino acids
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single;
TOPOLOGY: linear
US-08-478-435-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 FEGIDIYT 10
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FEGVAIYT 35
                                                               3 FEGIDIYT 10
                                                                                                       28 FEGVALYT 35
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66.7%; Score 34; DB 2; Length 36; 75.0%; Pred. No. 6.9; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Locsmore, Sheena
APPLICANT: Locsmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Harkness, Robin
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Silite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Suite CITY: Toronto STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ontario
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RESULT 9 US-08-337-483-19

Canada

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Length 36;
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; Sequence 19, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Gray-Owen, Scott
APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
APPLICANT: Murdin, Andrew
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
ITILE OF INVENTION: 1 Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSE: Sim & McBurney
STREET: Suite 701, 330 Unviersity Avenue
CITY: Toronto
CONTRESSE ONLERIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,577A
FILING DATE: 07-704-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-465 MIS:VG
TELEFONMUNICATION INFORMATION:
TELEFONDE: (416) 595-1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 3;
Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
      APPLICATION NUMBER: US/08/474,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 36 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 FEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 FEGVAIYT 35
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COUNTRY: Canada
ZIP: MSG 1R7
                                       FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY:
US-08-474-671-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
COMPUTER: Canada

CIP: MAGG IR7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,373

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/37,483

FILING DATE: 29-DEC-1994

FILING DATE: 29-DEC-1994

FILING DATE: 29-DEC-1993

APPLICATION NUMBER: US 08/175,116

FILING DATE: 08-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: STEWARTION:
NAME: STEWARTION:
NAME: STEWARTION:
NAME: STEWARTICN:
NAME: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: POSTEM: FO-mogatible
OPERATING SYSTEM: FO-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Murdin, Andrew
APPLICANT: Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
GITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1038-463 MIS:vg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/08474671
Patent No. 6008326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INPORMATION FOR EQU ID NO: 19:
SEQUIENCE TERRACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 FEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: LOOSMON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-478-373-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-474-671-19
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APPLICANT: LOOSMOTE, Sheena M
APPLICANT: LOOSMOTE, Robin E
APPLICANT: Schryvers, Anthony B
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Wardin, Andrew D
APPLICANT: Yang, Yan-Ping
CORRESPONDENCES: 147
CORRESPONDENCE SIM & MCBurney
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: IB
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                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,654
FILING DATE: US-AUG-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA94/00616
FILING DATE: ATTORNEY: ACTORNATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 3
Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/08637654
Patent No. 6358727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFRENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 anino acids
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPAX: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 FEGIDIYT 10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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TOPOLOGY:
US-08-897-438-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-637-654-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-08-897-438-19
US-08-897-438-19
; Sequence 19, Application US/08897438
; Patent No. 6262016
; Patent No. 6262016
; APPLICANT: Loosmore, Sheena APPLICANT: Ghorg, Pele APPLICANT: Chong, Pele APPLICANT: Chong, Pele APPLICANT: Wang, Yan-Ping APPLICANT: Klein, Michel TTIME OF INVENTION: Transferrin Receptor Genes NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSER: Sim & McBurney STREET: Ghordario STREET: Ch Floor, 330 University Avenue CITY: Toronto STREET: Charaio
STREET: Charaio
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IEM PC Compatible
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/897,438
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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CLASSIFICATION: 435
PRIOR PAPELICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/483,577
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/37,483
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 28-DEC-1993
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
          FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-511
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
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Best Local Similarity 75.0%;
Matches 6; Conservative
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; TOPOLOGY: linear
US-08-483-577A-19
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   Indels
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GENERAL INFORMATION:
APPLICANT: LOGGOMORE, Robin
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen Scott
APPLICANT: Gray-Owen Scott
APPLICANT: Gray-Owen Scott
APPLICANT: Gray-Owen Scott
APPLICANT: Murdin, Andrew
APPLICANT: Andrew
APPLICANT: Andrew
APPLICANT: Canada
ZIP: MURGSEE: Sim & McBurney
STREET: 6th Floor, 330 Unviersity Avenue
CITY: Toronto
STARE: One Ario
COUNTRY: Canada
ZIP: MGG 187
COMPUTER READABLE FORM:
MEDIUM TYPE FLOORS/MG-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
COMPUTER: LIBR PC Compatible
COMPUTER: LIBR PC Compatible
COMPUTER: 17-MAY-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/43,577
FILING DATE: 09-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 09-NOV-1993
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
TELEFORMURICATION INFORMATION:
TELEFORMURICATION INFORMATION:
TELEFORMURICATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DO
      ü
   1; Mismatches
                                                                                                                                                                                                         RESULT 15
US-08-649-518-19
; Sequence 19, Application US/08649518
; Patent No. 6361779
6; Conservative
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STRANDEDMESS: single
FOPOLOGY: linear
US-08-649-518-19
                                                         3 FEGIDIYT 10
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APPLICANT: LOOSMOI
Matches
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Search completed: September 15, 2004, 10:36:50 Job time : 16.7895 secs
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

September 15, 2004, 10:29:20; Search time 53.1579 Seconds (without alignments) 53.153 Million cell updates/sec Run on:

US-09-673-795-2 51 score: Title: Perfect

SLFEGIDIYT 10 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* geneseqp2004s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

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SUMMARIES	ID	AAY44200	AAB97602	AAB97603	ABR82812	ABM73781	AAY88410	AAY88413	AAY88409	AAY88412	AAB23252	AAR03930	AAR03929	AAW10065	AAY88408	AAY88411	AAB23653	ADD14137	AAR43004	AAW54349	AAB23652	AAB82534	AAE12986	ABU89711	ABR40398	ABR40397
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	Score	51	51	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47
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	Abr40399 Bovine HS	Abr40400 Human HSn			Rat	Rat	Hima	_									٠.	The contract of	٠.	Dro
	ABR40399	ABR40400	ADD46498	ADE57092	ADD45046	ADD47457	ADD47459	ADE76981	AAB23650	ABG93094	ABR52671	ABR52761	AAR03928	ABR40401	ABR40402	AAY44199	AAB97601	ABG79108	ADC97498	ABB71708
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Ç	97	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Heat shock protein 70 amino acid residues 286-295. AAY44200 standard; peptide; 10 AA. 15-FEB-2000 (first entry) AAY44200; 

Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; immune defence; immunogenicity; specificity; human leucocyte antigen.

Homo sapiens

WO9954464-A1.

28-OCT-1999.

99WO-FR000957. 22-APR-1999; 98FR-00005033. 22-APR-1998;

(INSR ) INST ROUSSY GUSTAVE.

Gaudin C; Triebel F, WPI; 2000-013251/01.

Identifying mutant peptides from heat-shock protein 70, for treatment of cancer.

Claim 10; Page 6; 56pp; French.

This peptide corresponds to amino acid residues 286-295 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce encoding DNA from one or more tumour-specific T cell response, comprises: (i) amplifying hsp70 sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer,

Sequence 10 AA;

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the amino acid sequence of fragment 2 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes or cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen the pericellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or intracellular infected cells.
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particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may also be used to increase the proportion of tumour-specific cytocoxic T lymphocytes in a cell culture and/or induce these cells to secrete cytocoxic factors (specifically interleukin-2, interferon-gamma and timmour necrosis factor), particularly where the cells are used to stimulate immunodenicity and high specificity for particular Hund.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 2.
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                               100.0%; Score 51, DB 3; Length 10; 100.0%; Pred. No. 0.00091; rive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB97602 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 15; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-SEP-2000; 2000WO-EP009530.
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                                                                                                                                                                                                                                                                           10; Conservative
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                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                  Sequence 10 AA;
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the amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membranes Recognition of increased numbers of HSP epitopes or cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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                                                                                                                                                                                                                                                                                                                                  HSP, HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 3.
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                                   Gaps
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                                   ;
100.0%; Score 51; DB 4; Length 10; 100.0%; Pred. No. 0.00091; ive 0; Mismatches 0; Indels
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Pred. No. 0.0062;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                 Heat shock protein 70 (HSP70) peptidic fragment 3.
                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.
                                                                                                                                                                                               AAB97603 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 15; 21pp; English.
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                    ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity
Matches 9; Conserv
   Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                     30-JUL-2001
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SLFEGIDEYT 10

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Sequences ABR82793-835 represent 43 overlapping peptide fragments of human heat-shock protein 70 (hsp70). The hsp70 peptides provide reliable differentiation between diabetes types I and II. The peptides induce a shift of the T cell response from Th1 (proinflammatory) to Th2 autoimmune diseases, especially type I diabetes but also systemic lupus autoimmune diseases, especially type I diabetes but also systemic lupus erythematosus, multiple sclerosis and rheumaroid arthritis; and (b) for diagnosing presence or onset of these diseases. Isolated T cells may be activated in vitro with (A), or with heat-shock protein 70 and the responding cells are selected, attenuated and then returned to the
                                                                                                                                                Heat-shock protein 70; hsp70; antidiabetic; human; immunosuppressive;
dermatological; antiinflammatory; neuroprotective; antirheumatic;
antiarthritic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides from human heat-shock protein 70, useful for treatment, prevention and diagnosis of autoimmune disease, specifically type I
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Pred. No. 0.014;
0; Mismatches 1; Indels
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                                                                                                                  Human hsp70 peptide p20 (residues 286-305).
                                                                                                                                                                                                                                                                                                                                                        (HADA-) HADASIT MEDICAL RES SERVICES & DEV. (YEDA ) YEDA RES & DEV CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                        Cohen IR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABM73781 standard; protein; 438 AA.
                           ABR82812 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 33; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                               24-FEB-2003; 2003WO-IL000143
                                                                                                                                                                                                                                                                                                                            26-FEB-2002; 2002IL-00148401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0s,
Best Local Similarity 90.0s,
                                                                                      (first entry)
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                                                                                                                                                                                                                                       WO2003072598-A2.
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                                                                                                                                                                                                           Homo sapiens
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                                                                                      18-DEC-2003
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                                                         ABR82812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetes
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ID ABM
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Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                          Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of barley varieties and production of barley transformants with desired
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90.0%; Pred. No. 0.45;
live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY88410 standard; protein; 554 AA.
                                                                                                                                                              20-DEC-2001; 2001JP-00387131.
20-DEC-2001; 2001JP-00403299.
20-DEC-2001; 2001JP-00403309.
27-SEP-2002; 2002JP-00337915.
                                                                                                                                                                                                                                                                    Kohara Y;
                                                                                                                   16-DEC-2002; 2002WO-IB005403
                                                                                                                                                  2001JP-00387059
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Best Local Similarity 90.00,
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                                                                                                                                                                                                                                                                   Takeda K,
                             Hordeum vulgare.
                                                         WO2003057877-A1.
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                                                                                                                                             20-DEC-2001;
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Sequence 554 AA;

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Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
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                                                                                                                                 Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
                                                                                                                                                                                                                  This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome
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                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 3; Length 554;
Pred. No. 0.58;
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                                                                                                                                                                                        Disclosure; Fig 3; 11pp; Japanese.
                                               (HOKE-) HOKEN KAGAKU KENKYUSHO KK
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                                                                                    2000-264458/23.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   Sequence 554 AA;
                                                                                                    N-PSDB; AAA15622
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Score 47; DB 3;
Pred. No. 0.58;
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    92.2%;
90.0%;
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Best Local Similarity
Matches 9; Conserv
              Local Similarity
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    Query Match
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Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.
             shock protein; HSP70; chromosome 6p21.3-22; stress;
                         chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 3; Length 554;
Pred. No. 0.58;
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90.0%;
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Best Local Similarity 90.00,
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                                                                                                                                                                                                                   WPI; 2000-264458/23.
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 554 AA;
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                                                                sapiens
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                heat
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              Human;
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The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a call which wereaxpresses Hsp72 (heat shock protein 71), and determining if the test compound inhibits activity or expression of Hsp72.

Conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp72-mediated JNK phosphatase comprising a contacting a test compound with a cell which expresses Hsp72, exposing the cell to a heat induced stress and determining if the compound inhibits JNK phosphatase activity. The invention additionally encompasses compositions comprising an inhibitor of Hsp72 or JNK phosphatase activity are useful for inhibiting the phosphatase activity are useful for inhibiting the phosphatase or Hsp72 or JNK phosphatase activity are useful for inhibiting the phosphatase or Hsp72 is used to treat a proliferative disorder such as carcinomas, breast cancer, prostate cancer). The compounds that inhibit they can also be administered to real premalignant conditions and to prevent progression to a neoplastic or malignant state. The compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient cancer intim a disease or disorder mediated by an increase of Hsp72 expression to man Hsp72 used in the exemplifications of the invention
                               Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia, lymphoma.
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                                                                                                     Example; Fig 16B; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus HSP (chkhsp70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88US-00243474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 634
N-PSDB; AAA97541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 624 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CODO-) CODON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-1988;
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Gaps

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Sias S;

Faulds D,

Dragon E,

WPI; 2000-647056/62.

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Bacillus megaterium (Bmehsp70 - AAR03923); 3. E. coli (dnaK - AAR03924); 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus (rathsp70 - AAR03927); 7. Xenopus laevis (x170 - AAR03928); 8. Homo sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930); 10. Zea mays (mzehsp70 - AAR03931); 11. Serratia marcescens (smahsp70 - AAR03932). The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                                         Mycobacteria species
                                                                                                                                   Sequence 640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
AAY88408
                                                                                                                                                                                                                                                                                         RESULT 13
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                                                                                                                     According to the legend of Fig 2, the G. gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "O" (?) at position 634. Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.hyoneumoniae (Mhyhsp70 - AAR03922); 2. Bacillus megaterium (Bmehsp70 - AAR03923); 3. B. coli (dnaK - AAR03924); 4. T. cruzi (AAR03926); 6. Rat ratus (rathsp70 - AAR03929); 7. Xenopus laevis (x170 - AAR03928); 8. Homo sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930); 10. Zea mays (mzehsp70 - AAR03931); 11. Serratia marcescens (smahsp70 - AAR03931) AAR03932). The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - used in
                                                   Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins homologous to heat shock proteins of Trypanosoma cruzi - used avaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
                                                                                                                                                                                                                                                                                                                             Score 47; DB 2; Length 634;
Pred. No. 0.68;
                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2.1-2.14; 86pp; English.
                                                                                                Disclosure; Fig 2.1-2.14; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR03929 standard; protein; 640 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88US-00243474.
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                                                                                                                                                                                                                                                                                                                                      92.2%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
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                                                                                                                                                                                                                                                                                 Mycobacteria species
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                             WPI; 1990-115820/15
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                            Sequence 634 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load.
                                                                                                                                                                                                                                                                                                                                                                                                           Human; heat shock protein 70; HSP70; primer; probe; detection; intracellular; abnormal transcription; acute; chronic; sustained; stress.
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Score 47; DB 2; Length 640;
Pred. No. 0.69;
0; Mismatches 1; Indels
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90.0%; Pred. No. (
                                                                                                                                                                                                                                          AAW10065 standard; protein; 640 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95JP-00158581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95JP-00158581
        92.2%;
90.0%;
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           Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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95JP-00158581

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Search completed: September 15, 2004, 10:34:09 Job time : 54.6579 secs
        01-JUN-1995;
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                                                                                                                                                                                                                                                                                                                    Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the human heat shock protein HSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                            Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; LHSP70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.2%; Score 47; DB 3; Length 640; 90.0%; Pred. No. 0.69; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human heat shock protein LHSP70 amino acid sequence.
                                                                    Human heat shock protein HSP70 amino acid sequence.
AAY88408 standard; protein; 640 AA
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                                                                                                                                                                                                                                                             (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 1; 11pp; Japanese.
                                                                                                                                                                                                                99JP-00257146.
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                                               (first entry)
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                            Homo sapiens
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                                               31-JUL-2000
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                                                                                                 Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
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Pred. No. 0.69;
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(HOKE-) HOKEN KAGAKU KENKYUSHO KK
                                                                                                                                                                        Disclosure, Fig 4; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Query Match
Best Local Similarity 90.00,
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                                                 WPI; 2000-264458/23
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DO ONK

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Q8uwm9 xiphophorus
Q9u667 littorina s
Q9u669 littorina s
Q9u669 littorina s
Q9u661 littorina s
Q9u666 littorina p
Q9u666 littorina p
Q9u668 littorina p
Q9u668 littorina p
Q9u689 littorina p
P81159 aplysia cal
Q980520 noncorhynchu
Q98899 fugu rubrip
Q8 jhm8 cetorhinus
Q8 jhm8 cetorhinus
Q8 jhm4 pseudocarch
Q8 jhm8 alopias sup
                                                    September 15, 2004, 10:30:46; Search time 32.6842 Seconds (without alignments) 86.882 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                     1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                              1017041 seqs, 315518202 residues
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                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                     - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8UWM9
Q9U667
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Q8JHN4
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sp_vorentebrate:*
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Gapop 10.0 , Gapext 0.5
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46
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No.
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pseudocarch	08 jhn5	Q8JHN5	13	462	91.3	42	45
	08jhs5	Q8JHS5	13	462	91.3	42	44
	Q8-jhp2	08ЛНР2	13	462	91.3	42	43
	08jht2	Q8JHT2	13	462	91.3	42	42
alopias	08jhr3	Q8JHR3	13	462	91.3	42	41
	08jhr9	Q8JHR9	13	462	91.3	42	40
	Q8jht1	Q8JHT1	13	462	91.3	42	39
	Q8jhn7	Q8JHN7	13	462	91.3	42	38
alopias	Q81h83	Q8JHS3	13	462	91.3	42	37
	08ins2	Q8JHS2	13	462	91.3	42	36
	OSTP	QBJHP1	13	462	91.3	42	35
naelidorarch	OBihne	08JHN6	13	462	91.3	42	34
aloniae nel	0811180	08JHS6	13	462	91.3	42	33
James ditro	0811110	OBJHR0	13	462	91.3	42	32
	75:103	OBJHT6	13	462	91.3	42	31
Jampa ditro	941 FBO	08JH09	13	462	91.3	42	30
	081bt4	Q8JHT4	13	462	91.3	42	29
	ORIDS	Q8JHS9	13	462	91.3	42	28
	OBibni	Q8JHN1	13	462	91.3	42	27
	081103	Q8JH03	13	462	91.3	42	26
	081hp4	08JHP4	13	462	91.3	42	25
	081hg0	Q8JHQ0	13	462	91.3	42	24
	081hg7	Q8JHQ7	13	462	91.3	42	23
	941-180	08JHP9	13	462	91.3	42	22
	081016	Q8JHR6	13	462	91.3	42	21
cetorhin	081hn3	08JHN3	13	462	91.3	42	20
	081hr8	QBJHRB	13	462	91.3	42	19
	081hr2	Q8JHR2	13	462	91.3	42	18
mitsukurina	504ihp3	08JHP3	13	462	91.3	42	17

## ALIGNMENTS

RESULT 1

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1 SLFEGIDIY 9

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Gaps

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Littorina scutulata (Checkered periwinkle).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
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Bukaryota, Metazoa, Mollusca, Gastropoda; Orthogastropoda;
Apogastropoda, Canogastropoda, Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
                                                       ;
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Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
"Heat-shock genes in the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AFP191830; AAF12789.1; -.
IGNE, AG005524; F.AFP binding; IFA.
InterPro; IPR001023; HSp70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Heat-shock genes in the heat-stressed genus Littorina."; submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AF191826; AAF12785.1; ---
GO, GO:0005224; F.APP binding; IEA.
InterPro; IPR01023; HSp70.
ProDom; PD000089; HSp70, 1.
PROSITE; PS01036; HSp70, 1.
ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 155;
       91.3%; Score 42; DB 5; Length 153; 88.9%; Pred. No. 1.8; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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155
17676 MW; C191F6E5B1F346C2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                        01-NAY-2000 (TrEMBLrel. 13, Created) 01-NAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 1.8;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heat-shock protein (Fragment).
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88.9%;
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Best Local Similarity 88..
88..
8; Conservative
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               Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                             80 SLFEGIDFY 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 AA;
                                                                                                             1 SLFEGIDIY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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Q9U665,
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Q9U669
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Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
                                                                                                                                                                                                                                                                                       Littorina plena (Black periwinkle).
Bukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Carperopoda, Sorbeoconcha, Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hoberlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
"Heat-shock genes in the heat-stressed genus Littorina.";
submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; AF191825; AAF12784.1; --
GO; GO:0005524; F:AFP binding; IEA.
InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70.
ProDom; PD000089; HSP70.
ProDom; PD000089; HSP70.3; 1.
ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hohenlohe P.A.;
"Hear-shock genes in the heat-stressed genus Littorina.";
submitted (OCT-1999) to the BMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AF191828; AAF12787.1; -.
GO, GO:005524; F:ATP binding; IEA.
InterPro; IPR001023; Hep70.
Pram; PF00012; HSP70; 1.
PROSOUR; PS00089; HSP70; 1.
ATP-binding.
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153 153
153 AA; 17352 MW; E29EE20C4CAF934D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 AA; 16607 MW; C3F3556A1AF438BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                         090667;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat-shock protein (Fragment).
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                                                                                                                       146 AA
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                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heat-shock protein (Fragment).
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hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                       PRELIMINARY;
288 SLFEGVDLY 296
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                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=31219;
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146
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ProDom; PD000089; Hsp70; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding.
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              [1]
SEQUENCE FROM N.A.
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                                                     Hohenlohe P.A.;
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Q9U668;
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Eukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
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Littorina plena (Black periwinkle).
Littorina plena (Black periwinkle).
Littorina plena (Black periwinkle).
Littoringta, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
NCBI_TaxID=31219,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                91.3%; Score 42; DB 5; Length 157; 88.9%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.3%; Score 42; DB 5; Length 158; 88.9%; Pred. No. 1.8;
                                                                                                                                                                                                                              1; Indels
                                                                                                  1 157 157 157 AA; 17834 MW; E8F743382B2BBB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 AA; 17887 MW; B41E5356A24CAD2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Heat-shock protein (Fragment).
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                                                                                                                                                                                                                          0; Mismatches
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HBATSHOCK70.
ProDom; PD000089; HSP70; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding.
1 1
NOW_TER 157 157
SEQUENCE 157 AA; 17834 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat-shock protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PP00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; HSP70; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                          8; Conservative
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                                                                                                                                                                                                                                                                                                    SLFEGIDFY 92
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Best Local Similarity
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SEQUENCE 15
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AC 2016
AC 2016
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DT 01-M
DT 01-C
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Enkaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
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"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the BMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
SONG GO:0005224; F.ATP binding; IEA.
InterPro; PR001023; HSP70.
Pfam: PF00012; HSP70;
PRINTS; PR00121; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 AA; 17868 MW; D2ECE71042EC44CB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat-shock protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.3%; Score 42; DB 5; ilarity 88.9%; Pred. No. 1.8; Conservative 0; Mismatches
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P81159
ID P8111
AC P8111
DT 01-J
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us-09-673-795-1.rspt

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                                                                       Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
                                                                                                                                              MEDLINE=93077669; PubMed=1360013; MEDLINE=93077669; PubMed=1360013; MEDLINE=93077669; PubMed=1360013; Minl D.; Kennedy T., Bazzilai A., Kandel E.; Ling-term sensitization training in Aplysia leads to an increase in the expression of BiP, the major protein chaperon of the ER."; O' Cell Biol. 119:1069-1076(1992).
--- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.
--- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Rainbow trout 70 kDa heat shock protein (Fragment).
Oncorbynchus mykiss (Rainbow trout) (Salmo gairdneri).
Actinopterygii, Meopterygii, Teleostei; Buteleostei;
Protacanthopterygii, Salmoniformes, Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A REDLINE-85036330; PubMed=6092938;

A MEDLINE-85036330; PubMed=6092938;

A Cochary R.K., Jones D., Candido E.P.M.;

To-kilodalton heat shock polypeptides from rainbow trout:

Therefore a result of cDNA sequences.";

Mol. Cell. Biol. 4:1785-1791(1984).

E. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

R. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

R. PIR; I51344; I51344.

R. PIR; I51344; I-HJO.

R. GO; GO:0005374; F:ATP binding; IEA.

R. GO; GO:0005374; F:ATP binding; IEA.

R. GO; GO:0005373; F:ATP binding; IEA.

R. InterProo; IPRO01021; HSp70.
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Pred. No. 2.6;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Heat shock cognate 71 kDa protein (Fragment).
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                                                           Aplysia californica (California sea hare).
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                                                                                                       Aplysioidea, Aplysiidae, Aplysia.
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PRINTS; PR00301, HEATBHOCK70.
ProDom; PD000089; HSP70, 1.
PROSITE; PS00329; HSP70_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
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                                                                                                                        NCBI_TaxID=6500;
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MEDIJINE=99284127; PubMed=10357235;

Lim E.H., Brenner S.; PubMed=10357235;

Lim E.H., Brenner S.;

Lim E.H., Brenner S.;

Comparisons of a cluster of five HSP70 genes in Fugu rubripes.";

Cell Mol. Life Sci. 55:668-678(1999).

-I - SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

EMBL; Y08578; CAA65092.1; --

HSSP; P19120; BHSC.

HSSP; P19120; BHSC.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Alopiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertébrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopororpha; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Takifugu.
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                                                                                                                                                          Length 278;
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                                                                                                    278 AA; 30327 MW; E4C745DE5484C17A CRC64;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003773; F:heat shock protein activity; IEA.
InterPro; IPR01023; Hsp70.
PRIMTS; PR00012; HSP70, 2.
ProDom; PR000089; Hsp70; 1.
PROSITE; PS00297; HSP70; 1.
PROSITE; PS01036; HSP70; 1.
PROSITE; PS01036; HSP70; 1.
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Last annotation update)
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-GT-2003 (TrEMBLrel. 25, Last annotation update)
70kD heat shock protein (Fragment).
                                                                                                                                                        Score 42; DB 13;
Pred. No. 3.4;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 AA
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PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                91.3%;
88.9%;
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                 Query Match
Best Local Similarity 88.50,
Best Local Similarity 88.70,
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                    ATP-binding; Heat shock.
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                                                                                278
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Best Local Similarity
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SEQUENCE
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Cetorhinus

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Blasmobranchii, Galeomorphii, Galeoidea, Lamniformes,
Pseudocarchariidae, Pseudocarcharias.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Alopiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Pska5;
Martin A.P., Burg T.;
"Perils of paralogy: Using Hsp70 genes for inferring organismal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phylogenies."

Lybylogenies."

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

-1 - SIMILARIYY BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

R GO; GO:005524; F:ATP binding; IEA.

InterPro; IPR0012; HSP70.

R PRINY: PR00312; HSP70.

R PROSITE; PS00329; HSP70.

R PROSITE; PS00329; HSP70.

R PROSITE; PS01036; HSP70.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.3%; Score 42; DB 13; Length 459; 88.9%; Pred. No. 5.8; tive 0; Mismatches 1; Indels
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-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AFS02452; AAM53160.1; -.
GO; GO:0005524; F:ATP binding; IEA.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
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Last annotation update)
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                                                                                                                  459 AA.
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                           Pseudocarcharias kamoharai.
                                                                                                                                                                                                                                                                  Hsp70 protein (Fragment).
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                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=57991;
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~ Q8JHN4;
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Q8JHS0
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                  Marrin A.P., Burg T., "Perils of paralogy: Using Hsp70 genes for inferring organismal
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                                                                                                                                                                                                            Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AFSO244; AAM53202.1; -.
GO; GO:0005524; F:AFP binding; IEA.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 91.3%; Score 42; DB 13; Length 444; Best Local Similarity 88.9%; Pred. No. 5.6; Matches 8; Conservative 0; Mismatches 1; Indels
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88.9%; Pred. No. 5.8;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 AA; 48889 MW; 7701945FBB99A2BA CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat shock rotein 70 (Fragment).
Rattus rattus (Black rat).
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InterPro; IPR001023; Hsp70.
Ffam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHCKTO.
PROSITE; PS00329; Hsp70; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0301; HEATSHOCK70.
PRODOM; PD000089; HSP70; 1.
PROSITE; PS00329; HSP70; 1.
ATP-binding.
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SEQUENCE 444 AA, 48889 MW; 7
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NCBI_TaxID=57982;
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RESULT 13
063718
1D Q63711
AC Q637115
AC Q637117
DT 01-NO

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Gaps

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DR ProDom; PD000089; Hsp70; 1.

DR PROSITE; PS00329; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_2; 1.

KW ATP-binding.

FT NOW_TER 461

SQ SEQUENCE 461 AA; 50591 MW; 1A9ESB4EC41077FE CRC64;

Query Match

Best Local Similarity 88.9%; Pred. No. 5.8;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 1 SLFEGIDIY 9

DD 246 SLFEGIDY 254

Search completed: September 15, 2004, 10:35:44

JOB time : 33.6842 secs
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

September 15, 2004, 10:30:21; Search time 8.05263 Seconds (without alignments) 58.196 Million cell updates/sec Run on:

US-09-673-795-1 46 1 SLFEGIDIY 9 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query	Length	DB	ID	Description
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S.	42	91.3	638	Н	HS71 CERAE	cercon
9	42	91.3	638	Н	HS72_YEAST	
7	42	91.3	639	н	HS71_ORYLA	_
8	42	91.3	639	Н	HS74_PARLI	
6	42	91.3	640	Н	HS7A_CAEEL	
10	42	91.3	640	Н	HS7C_DICDI	_
11	42	91.3	641	Н	HS71_BOVIN	
12	42	91.3	4	Н	HS71_HUMAN	
13	42	91.3	4	М		
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5	42	91.3	4	Н	HS71_YEAST	
91	42	91.3	4		HS72_BOVIN	
7.7	42	91.3	4		HS74_YEAST	Sac
20 (	42	91.3	せ		HS71_MOUSE	,
on (	42	91.3	4		HS70_BRUMA	
50	42	91.3	4		HS70 ONCTS	
27	42	91.3	51	Ч	HS70_PLEWA	
22	42	91.3	646	М	HS70 NEUCR	Q01233 neurospora
23	42	91.3	4	Н	HS72 SCHPO	
4.1	42	91.3	4.	H	HS70_XENLA	٠.
52	42	91.3	4	Н	HS70_BLAEM	blastocl
9 7	42	91.3	n	Н	HS7D MANSE	-
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3.2	41	89.1	₹*	Н	S76_H	
33	41	89.1	₹*	Н	HS76_PIG	

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Gaps

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th 91.3%; Score 42; DB 1; Length 322; Similarity 88.9%; Pred. No. 0.71; 8; Conservative 0; Mismatches 1; Indels

Query Match Best Local Similarity Matches 8; Conserv

420 AA.

PRT;

STANDARD;

RESULT 2 HS1A\_MOUSE ID \_HS1A\_MOUSE

51

43 SLFEGIDEY

1 SLFEGIDIY 9

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Q01877 puccinia gr P55063 rattus norv P34931 homo sapien P16627 mus musculu P53623 pichia angu Q10265 schizosacch P53421 pichia angu P27322 lycopersico P26413 glycine max P19378 cricetulus P11142 homo sapien P08109 mus musculu	OONCYO STANDARD; PRT; 322 AA.  OCT-1989 (Rel. 12, Created) STRE-1966 (Rel. 23, Last sequence update) STRE-1966 (Rel. 43, Last sequence update) STRE-196 (Rel. 43, Last sequence update) STRE-196 (Rel. 43, Last sequence update) STRE-196 (Rel. 43, Last shock protein 70 is a major immunogen in stetein N., Highesticol. 30:20-236(1989).  MINCELLANBOUS: Heat shock protein 70 is a major immunogen in stock protein 70 is a major in statement is not removed. Usage by and for commercial populos in statement is not removed. Usage by and for commercial field and this statement is not removed. Usage by and for commercial field and this statement is not removed. Usage by and for commercial reprovious profit in strengen 10 incenses is sentence 10 incenses is se
HS71_PUCGR HS1A_RAT HS7H HUMAN HS7T_MOUSE HS77_SCHPO HS71_SCHPO HS71_PICAN HS72_LYCES HS72_LYCES HS70_CRIGR HS7C_CRIGR HS7C_CRIGR HS7C_CRIGR HS7C_CRIGR HS7C_CRIGR HS7C_CRIGR HS7C_MOUSE	PRT; 322 A sequence update annotation upda iSP70) (Fragmen is Chromadorea; Yates J., Rajan tock protein 70 is Chroma filania from a filaria from a filaria from a filaria is not removed agreement (See is not removed is not removed is not removed is not removed agreement (See is not removed is not removed is not removed is not removed in the not removed in the not removed is not removed in the not removed is not removed in the not removed in the not removed in the not removed is not removed in the not removed in
88 88 88 48 40 70 70 70 70 70 70 70 70 70 70 70 70 70	ULT 1  0 ONCVO  HS70_ONCVO  HS70_ONCVO  HS70_ONCVO  HS81_ONCVO  HS81_S1, Last sequence upo  15-MAR2004 (Rel. 33, Last sequence upo  15-MAR2004 (Rel. 33, Last sequence upo  15-MAR2004 (Rel. 33, Last sequence upo  Heat shock 70 kDa protein (HSP70) (Freg  Onchocerca volvulus.  Bukaryota; Metazoa; Nematoda; Chromador  Onchocercidae; Onchocerca.  NCBI TaxID=6282;  SEQUENCE FROM N.A.  MEDLINE=89201313; PubMed=2704388;  Nochtstein N.M., Higashi G., Yates J., R  "Onchocerca volvulus heat shock protein  microfilaremic individuals from a fila  MOI Biochem. Parasitol 33:229-236(198  "Onchocerca volvulus heat shock protein  microfilaremic individuals from a fila  "Onchocerca volvulus heat shock protein  microfilaremic individuals from a fila  "Onchocerca volvulus seat shock protein  microfilaremic individuals from a fila  "Onchocerca volvulus seatement is not remo  onchities requires a license agreement (or send an email to license@isb-sib.ch)  EMBL; JOHO06; AAA29417.1; -  HSSP; POR0102; HSP70_1; PARTIAL.  PROSITE; PS00129; HSP70_1; PARTIAL.  PROSITE; PS00139; HSP70_1; PARTIAL.  PROSITE; PROSITE; PS00139; HSP70_1; PROSITE; PROSITE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.; "Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H., Molecular cloning and expression of a Penicillium citrinum allergen with sequence homology and antigenic crossreactivity to a hsp 70
                                                                                                                                                                                                                                                                      Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 261:12692-12699(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human heat shock protein.";
Clin. Exp. Allergy 27:682-690(1997).
-!- ALLENGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 503;
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                         16-0CT-2001 (Rel. 40, Created)
116-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last amotation update)
Heat shock 70 kDa protein (Allergen Pen c 19) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
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88.9%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probom; PD000089; HSp70.1; PRAFIIAL. PROSITE; PS00297; HSP70.1; PARTIAL. PROSITE; PS00329; HSP70.2; 1. PROSITE; PS01036; HSP70.2; 1. PROSITE; PS01036; HSP70.3; 1. NOW_TER 1. 1.
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01-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                634 AA.
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MEDLINE=86304452; Pubmed=3017985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97351908; PubMed=9208190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001023; HSp70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U64207; AAB06397.1; -. HSSP; P19120; 3HSC.
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                                                                                                                                                                                                                                        Penicillium citrinum.
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5077;
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HS70 CHICK
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SOLUTION NEW TAX TO THE PROPERTY OF THE PROPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Provided in cooperation with other chaperones, Hsp70s stabilize preexistent proteins against aggregation and mediate the folding of newly translated polypeptides in the cytosol as well as within organelles. These chaperones participate in all these processes through their ability to recognize nonnative conformations of other proteins. They bind extended peptide segments with a net hydrophobic character exposed by polypeptides during translation and membrane translocation, or following stress-induced damage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=86111900; PubMed=2868009;
Lowe D.G., Moran L.A.;
"Molecular cloning and analysis of DNA complementary to three mouse
Mr = 68,000 heat shock protein mRNAs.";
J. Biol. Chem. 261:2102-2112(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perry M.D., Aujame L., Shtang S., Moran L.A.; "Structure and expression of an inducible HSP70-encoding gene from
                                                                                                                                                                                                                                                                          Mus musculus (Mouse),
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                             01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Heat shock protein 1A (Heat shock 70 kDa protein 3) (HSP70.3)
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EMBL; M12572; AAA57235.1; -.
EMBL; M12572; AAA57235.1; -.
EMBL; M2583; AA56283.
HSSP; P08109; 1CKR.
MGD; MGI:96244; Hspala.
InterPro; IPR00122; Hsp70.
Pfam; PF00012; HSP70.1.
PRINTS; PR003031; HSP70.1.
PROSITE; PS002097; HSP70.1; PARTIAL.
PROSITE; PS0103029; HSP70.2; PARTIAL.
PROSITE; PS01036; HSP70.3; 1.
AMTP-binding; Chaperone; Heat shock; Multigene family.
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                                               Created)
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HSPA1A OR HSP70-3 OR HSP70A1.
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Gene 146:273-278(1994).
                                           01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
10-OCT-2003 (Rel. 42,
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420 AA;
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503 AA.

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STANDARD;

RESULT 3 HS70\_PENCI ID HS70\_PENCI

SEQUENCE Query Match

Matches Best

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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PRINTS; PR00301; HBATSHOCK70.

PROSITE; PS00299; HSP70; 1.

PROSITE; PS00329; HSP70; 1.

PROSITE; PS01036; HSP70, 2; 1.

PROSITE; PS01036; HSP70, 3; 1.

ATP-binding; Heat shock; Multigene family.

ATP-binding; Heat shock; Multigene family.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
16at shock 70 kDa protein 1.
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InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
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tes 8; Conserv
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15-DEC-1998
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STRAINS-2288C / AB972;
WEDLINE-97313267; PubMed-9169871;
WEDLINE-97313267; PubMed-9169871;
WEDLINE-97313267; PubMed-9169871;
ADDISTON M., Hiller L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Osffeau A., Hebling U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P., Louis B.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Scherrens B., Scholler P., Schwarz S., Onderwood A.P., Urrestarazu L.A., Vandenboll M., Verlassell F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The sequence of 32kb on the left arm of yeast chromosome XII reveal
six known genes, a new member of the seripauperins family and a new
ABC transporter homologous to the human multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Slater M.R., Craig E.A.;
"The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
Nucleic Acids Res. 17:805-806(1989).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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Pred. No. 1.4;
); Mismatches
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01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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or send an email to license@isb-sib.ch)
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MEDLINE=97197984; PubMed=9046100;
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                                                                                                           HSSP, P08107; 1100.

InterPro; IPR001023; HSp70.

Pfam; PP000121; HSP70. 1.

PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS00297; HSP70. 1.

PROSITE; PS00297; HSP70. 1; 1.

PROSITE; PS01036; HSP70. 2; 1.

PROSITE; PS01036; HSP70. 2; 1.

ATP-binding; Chaperone; Heat sho SEQUENCE 638 AA; 69920 MW; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . . 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.3%;
                                                        EMBL; X70684; CAA50019.1;
PIR; S31766; S31766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shock protein SSA2.
OR YLL024C OR L0931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Teast 13:183-188(1997),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 SLFEGIDFY 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 387:87-90(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SLFEGIDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
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HS72_YEAST
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SEQUENCE OF 91-97 AND 325-341.

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639 AA
              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.2
Local Similarity 88.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 SLFEGIDFY 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SLFEGIDIY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                             P08109; 1CKR.
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                         NCBI_TaxID=8090;
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                  ORYLA
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Q06248;
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                  HS71 OR'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
HS74 PARLI
HS71_ORYLA
                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                           "Protein expression during exponential growth in 0.7 M NaCl medium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                 MEDLINE=95203288; PubMed=7895733;
Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender E Volge T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein database.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- PTM: Phosphorylated.
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 1; Length 638;
Pred. No. 1.4;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HBATESHOCK70.
ProDom; PD000089; HSP70; 1.
PROSITE; PS00297; HSP70; 1.
PROSITE; PS00329; HSP70 2; 1.
PROSITE; PS01036; HSP70 2; 1.
Heat shock; ATP-binding; Multigene family; Acetylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GG:0009277; C:cell wall (sensu Fungi); IDA.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0000329; C:vacuolar membrane (sensu Fungi); IDA.
GO; GO:0003773; F:heat shock protein activity; IMP.
GO; GO:00006457; P:protein folding; IMP.
InterPro; IPR001023; Hsp70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACETYLATION.
23BDDD120C194912 CRC64;
                                                                                                                                                                                              Saccharomyces cerevisiae.";
FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                  Electrophoresis 15:1466-1486(1994).
                                                                                                                              STRAIN=ATCC 38531 / Y41;
MEDLINE=97089742; PubMed=8935650;
                                                                                                                                                                                                                                            ACETYLATION, AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X12927; CAA31394.1; -.
EMBL; Z73129; CAA97472.1; -.
EMBL; X97560; CAA66167.1; -.
PIR, S20139; S20139.
HSSP; P19120; 3HSC.
GermOnline; 142019; -.
SWISS-2DPAGE; P10592; YEAST.
COMPLUYEAST-2DPAGE; P10592; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           638 AA; 69338 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.3%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.5.,
Best Local Similarity 88.5.
                                                                                                                                                                 Norbeck J., Blomberg A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 SLFEGIDFY 290
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                                                                                                                    SEQUENCE OF 186-195.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzinas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] — MEDQUENCE FROM N.A. MEDGUINCE 9309705; MEDLINE=93077053; PubMed=1339375; Sconzo G., Scardina G., Ferraro M.G.; Sconzo G., Scardina G., Ferraro M.G.; Characterization of a new member of the sea urchin Paracentrotus lividus hap70 gene family and its expression."; Gene 121:553-258(1992). -- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .<del>.</del>
                                                                                                                                                                                                                                                                                                                                                         Naruse K., Sakuragi M.;
"Medaka HSP70 gene cloning.";
submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1; Length 639;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; ISR001023; HSP70.

Pfam; PF00012; HSP70; 1.

PRINTS; PR00301; HEATSHOCKTO.

ProDon; PE000089; HSP70; 1.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Heat shock; Multigene family.

SEQUENCE 639 AA; 70350 MW; 610B7E0DCGEE0534 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Heat shock 70 kDa protein IV (HSP70 IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        639 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paracentrotus lividus (Common sea urchin).
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88297155; PubMed=2841196;
Snutch T.P., Heschl M.F.P., Baillie D.L.;
"The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 64:241-255(1988).
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                    91.3%; Score 42; DB 1; Length 639; 88.9%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                      HSSP, P19120; 3HSC.

InterPro; IPR001023; HSp70.

Pfam; PP00012; HSP70.

PRONTS: PR001031; HSP70.

PROSITE; PS00297; HSP70; 1.

PROSITE; PS001329; HSP70 1; 1.

PROSITE; PS01329; HSP70 2; 1.

PROSITE; PS01036; HSP70 3; 1.

PROSITE; PS01036; HSP70 3; 1.

ATP-binding; Heat shock; Multigene family.

SEQUENCE 639 AA; 69749 MW; 40E2F29570806DCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000089; Hsp70; 1.
PROSTTE; PS00297; HSP70_1; 1.
PROSTTE; PS01036; HSP70_2; 1.
PROSTTE; PS01036; HSP70_2; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Heat shock 70 kDa protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    640 AA
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0; Mismatches
                                                                                                                                      EMBL; X61379; CAA43653.1; -. PIR; JC1391; JC1391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M18540; AAA28078.1; -.
PIR; JT0285; HHKW7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P19120; 1HPM.
InterPro; IPR001023; HSp70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 SLFEGIDFY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SLFEGIDIY 9
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
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MEDLINE=940431116; PubMed=8226849;

Eddy R.J., Sauterer R.A., Condeelis J.S.;

T. "Aginactin, an agonist-regulated Factin capping activity is associated with an HSC70 in Dictyostellum.";

J. Biol. Chem. 268:23267-23274(1993).

T. FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN-BINING PROTEIN CAP23/34. ACTS AS A CHABERONE BY STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.

T. SUBGELIULAR LOCATION: Cytcolnasmic. Found in F-actin-rich regions of the cell cortex and cell protrusions.

C. DEVELOPMENTAL STAGE: Heat shock cognate proteins are expressed constitutively during normal development.

C. SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSSIGIDLGTTYSCVGVWQNDRVEIIAND -> IHHHINGNATWVVESGPVSEVLSFN (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94008983; PubMed=8404847; Hartmann H., Lottspeich F., Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F., Noegel A.A., Schleicher M.; "The heat shock cognate protein from Dictyostellum affects actin Polymerization through interaction with the actin-binding protein
                                                                           .
0
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SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309
             Length 640;
                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
   91.3%; Score 42; DB 1;
88.9%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                            640 AA
                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heat shock cognate protein (Aginactin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                                            PRT;
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HSSP, 291394; 337394.

HSSP, 219120; 3HSC.

SWISS-2DPAGE; P36415; DICTY.

DictyBasse; DDB0001837; hspB.

InterPro; IPR001023; hspP0.

PRINTS; PR00301; HSP70; 1.

PROSITE; PS00295; HSP70; 1.

PROSITE; PS00295; HSP70; 1.

PROSITE; PS00295; HSP70; 1.
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                                                                 8; Conservative
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                                                                                                                                                                                       287 SLFEGIDFY 295
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                                                                                                                            1 SLFEGIDIY 9
Query Match
Best Local Similarity
Matches 8; Conserv
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P36415;
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PIR; S53357; S53357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HERPO-1) locus.)

Anim. Genet. 25:196-1994).

PRESTIGENT IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
-!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
-!- FUNCTION: IN COOPERATION WITH OTHER CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE BROPLASHIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE POR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECORDIZE NONMATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PRETIDE SEGMENTS WITH A NET HYROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gutierrez J.A., Guerriero V.; "Chemical modifications of a recombinant bovine stress-inducible 70 KDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues."; Biochem. J. 305:197-203 (1995).
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Angus;
MEDLINE=95030563; PubMed=7943958;
Grosz M.D., Skow L.C., Stone R.T.;
"An Alul polymorphism at the bovine 70 kD heat-shock protein-1
                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRESS-INDUCED DAMAGE.
INDUCTION: By heat shock.
SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                          91.3%; Score 42; DB 1; Length 640; 88.9%; Pred. No. 1.4;
                                                                                                                                     Indels
 N -> T (IN REF. 2).

N -> A (IN REF. 2).

N -> A (IN REF. 2).

S -> A (IN REF. 2).

V -> A (IN REF. 2).

V -> D (IN REF. 2).

F -> P (IN REF. 2).

ZEGBDC2DB96A9FSD CRC64;
                                                                                                                                     1;
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                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-95126904; PubMed=7826329;
                                                                                                                                     0;
   M H C O M C N
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                                                                                      70499 MW;
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                                                                                                                                      8; Conservative
     32
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640 AA;
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Matches 8; Conserv
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TISSUB-Muscle, Parcreas, and Skin; MISCUB-Muscle, Parcreas, and Skin; MEDLINE=22388257; PubMed=12477932; Straubsberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Straubsberg R.L., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Shiina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=66016721; PubMed=3931075;
Hunt C., Morimoto R.I.;
"Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";
Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lasky S., Hood L.; "Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Milner C.M., Campbell R.D.; "Structure and expression of the three MHC-linked HSP70 genes."; Immunogenetics 32:242-251(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A., Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J., Lasky S., Hood L.;
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1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H871 HUMAN STANDARD; PRT; 641 AA.
P08107; P19790; Q9UQL9; Q9UQM0;
P08107; P19790; Q9UQL9; Created)
01-FEB-1994 (Rel. 08, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
Heat shock 70 ke protein 1 (HSP70.1) (HSP70-2).
(HSPALA OR HSPAL) AND HSPALB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                              shock; Multigene family.; 6D548263E98780F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 1
Pred. No. 1.4;
0; Mismatches
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                                                                                           PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; Hep70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat sk
                                                                                                                                                                                                                                                                                                    70250 MW;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
HSSP; P08107; 1HJO.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 SLFEGIDFY 294
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                                                                                                                                                                                                                                                                                                        641 AA;
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I -> V (IN REF. 2).
E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 2).
MISSING (IN REF. 2).
N -> S (IN REF. 3; AAD21815).
                                                                                                 MIM; 603012; -.

R GO; GO:0005634; C:roytoplasm; TAS.

R GO; GO:0005634; C:roytoplasm; TAS.

R GO; GO:0005634; C:roytoplasm; TAS.

R GO; GO:0006402; P:mRNA catabolism; TAS.

R THCEYPO: IPRO01023; HSp70.

R PFLOM; PP00012; HSp70.

R PFLOM; PP000089; HSp70; 1.

R PRINTS; PR0031; HSP70; 1.

R PROSITE; PS00239; HSP70; 1.

R PROSITE; PS00136; HSP70.

R PROSITE; PS01036; HSP70.

R PROSITE; PS01036
                  SWISS-2DPAGE; P08107; HUMAN.
                                        Genew; HGNC:5232; HSPA1A.
Genew; HGNC:5233; HSPA1B.
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108
110
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CONFLICT
CONFLICT 31
CONFLICT 37
CONFLICT 46
CONFLICT 46
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MEDLINE=99234376; PubMed=10216320;

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MEDLINE=99234376; PubMed=10216320;

MEDLINE=99234376; PubMed=10216320;

MEDLINE=99234376; PubMed=10216320;

MEDLINE:

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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Nadan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-22 AND 618-641 FROM N.A.
MEDLINE=87066768; PubMed=3786141;
Drabent B., Genthe A., Benecke B.-J.,
"In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";
Nucleic Acids Res. 14:8933-8949(1986).
                                                                                                                                                                                                                                                              SEQUENCE OF 1-36 AND 360-424 FROM N.A.
MEDLINE=89184548; PubMed=2538825;
Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
"Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";
Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDUCTION: By heat shock. SIMILARITY: Belongs to the heat shock protein 70 family.
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AF134726; AAD21816.1;
AP000503; BAB63300.1;
AP000503; BAB63399.1;
MI717; AAA52697.1;
BC002453; AAH02453.1;
BC009322; AAH09322.1;
BC018740; AAH18740.1;
MA24744; AAA5944.1;
XO4677; CAA28381.1;
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EMBL; M59830; AAA63227.1; -.
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, A29160; A29160. ; A45871; A45871. ; I59139; I59139. ; I79540; I79540. 1HJO; 21-0CT-98

EMBL; EMBL;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preexistent proteins against aggregation and mediate the folding of newly translated polypeptides in the cytosol as well as within organelles. These chaperones participate in all these processes through their ability to recognize nonnative conformations of other proteins. They bind extended peptide segments with a net hydrophobic character exposed by polypeptides during translation and membrane translocation, or following stress-induced damage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete nucleotide sequence of a porcine HSP70 gene.";
Immunogenetics 35:286-289(1992)
-!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDILIBE-92175874; PubMed=1339404; MEDILIBE-92175874; PubMed=1339404; Pee-lman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J., Bouquet Y.H.;
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                                                                            Length 641;
                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ne, Heat shock; Multigene family. 70083 MW; FE77BB20A03E0A33 CRC64;
                                                                              Score 42; DB 1;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Heat shock 70 kDa protein 1 (HSP70.1).
                                                                                                               0; Mismatches
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PIR; S35718; S35718.
HSSP; P08107; 1HJO.
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Pfam; PP00012; HSP70, 1.
PRINTS; PR00301; HEAPSHOCK70.
ProDom; PD000089; HSp70; 1.
PROSITE; PS00297; HSP70 1:
PROSITE; PS00139; HSP70 2; 1.
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                                                                            91.3%;
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les 8; Conserv
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286 SLFEGIDFY 294

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hsp70 gene.";
Biochim. Biophys. Acta 1219:64-72(1994).
Biochim. Biophys. Acta 1219:64-72(1994).
In cooperation with other chaperones, Hsp70s stabilize preexistent proteins against aggregation and mediate the folding of newly translated polypeptides in the cytosol as well as within of newly translated polypeptides in the cytosol as well as within organelles. These chaperones participate in all these processes through their ability to recognize nonnative conformations of other proteins. They bind extended peptide segments with a net hydrophobic character exposed by polypeptides during translation and membrane translocation, or following stress-induced damage.
-!- INDUCTION: By heat shock.
                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=LBW 1W/GIN;
MEDLINE=95012453; PubMed=7927536;
Walter L., Rauh F., Guenther E.;
"Comparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:325-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J., Massa S.M., Sharp F.R., "cDNa cloning and expression of stress-inducible rat hsp70 in normal and injured rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE-94368874; PubMed-8086479;
Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.;
"Cloning, nucleotide sequence and expression of rat heat inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001023; Hsp70.
Pfam; PF00012; Hsp70. 1.
PRINTS; PR00301; Hsp70; 1.
PROSTIE; PS00209; Hsp70; 1.
PROSTIE; PS00209; HSP70; 1.
PROSTIE; PS00329; HSP70; 1.
PROSTIE; PS01036; HSP70; 1.
HS71_RAT STANDARD; PRT; 641 AA. 007439; P428B3; CECated) 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Heat shock 70 kDa protein 1/2 (HSP70.1/2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Neurosci. Res. 36:325-335(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94096443; PubMed=8271311;
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EMBL; X77209; CAA54423.1; --
EMBL; X77201; CAA54422.1; --
EMBL; X74271; CAA5328.1; --
PIR; I54542; I54542.
HSSP; P08107; IHJO.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=S286 / AB972;
MEDLINE=95028152; PubMed=7941740;
MEDLINE=95028152; PubMed=7941740;
Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
"Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
Yeast 10:335-541(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Slater M.R., Craig E.A., "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae."; Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S., "Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 590-641 FROM N.A.
MEDLINE-85087943; PubMed-6096826;
Ogden R.C., Lee M.-C., Knapp G.;
"Transfer RNA splicing in Saccharomyces cerevisiae: defining the
                                                                                                                                   0;
                                                                                       Score 42; DB 1; Length 641;
Pred. No. 1.4;
                                                                                                                                 Indels
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  D -> H (IN REF. 2 AND 3).
G -> A (IN REF. 3).
; D02D96751C868583 CRC64;
                                                                                                                                                                                                                                                                                                                                                          01-UUL-1989 (Rel. 11, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Heat shock protein SSA1 (Heat shock protein YG100).
SSA1 OR YALOGSC.
                                                                                                                                                                                                                                                                                                                           641 AA
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                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Electrophoresis 15:1466-1486(1994)
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MEDLINE=89128457; PubMed=2644626;
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MEDLINE=97089742; PubMed=8935650;
                                              70163 MW;
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                                                                                       91.3%;
                                                                                                         88.98;
                                                             Query Match
Best Local Similarity 86.>
Feet Local 8; Conservative
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641 AA;
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CONFLICT
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P10591;
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GO; GO:000277; C:cell wall (sensu Fungi); IDA.

GO; GO:0005737; C:cell wall (sensu Fungi); IDA.

GO; GO:0005737; C:cell wall

GO; GO:0005834; C:nucleus; IDA.

GO; GO:0016887; F:ATPase activity; IDA.

GO; GO:0016887; F:ATPase activity; IDA.

GO; GO:0006457; P:protein folding; IDA.

GO; GO:0000665; P:protein-nucleus import, translocation; IDA.

GO; GO:0000666; P:protein-nucleus import, translocation; IDA.

GO; GO:000061; P:Protein-nucleus import, translocation; IDA.

GO; GO:000061; P:Protein-nucleus import, translocation; IDA.

GO; GO:00006123; HSP70.
Volpe T., Warner J.R., McLaughlin C.S.;
submitted (SEP-1994) to Swiss-Proc.
-!- PUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
SSA1 AND SSA2 PROTEINS IS PREDETED. SSA1 CAN PARTICIPATE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: Belongs to the heat shock protein 70 family.
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Heat shock; ATP-binding; Multigene family; Acetylation.
INIT_MET 0
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88.9%; Pred. No. 1.4;
iive 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X12926; CAA31393.1; -.
EMBL; L22015; AAC04952.1; ALT_SEQ.
PIR; S43449; HHBYA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P19120; 3HSC. -
GermOnline; 138348; -
SMSS-2DPAGE; P10591; YEAST.
COMPLUYEAST-2DPAGE; P10591; -.
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PRINTS; PR00301; HEATSHOCK70.
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PROSITE, PS00297; HSP70 1; 1
PROSITE; PS00329; HSP70 2; 1
PROSITE; PS01036; HSP70 3; 1
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

September 15, 2004, 10:31:26; Search time 11.3684 Seconds (without alignments) 76.152 Million cell updates/sec Run on:

US-09-673-795-1 46 SLFEGIDIY 9 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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# ALIGNMENTS

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		-time molecular character House
5	51	41,770

dnaK-type molecular chaperone HSC70 - California sea hare (fragment)
NyAlternate names: heat shock protein 70 homolog HSC70
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999
C;Accession: B44261
B;Kuhl, D:, Kennedy, TE.; Barzilai, A.; Kandel, B.R.
J. Cell Biol. 119, 1069-1076, 1992
A;Title: Long-term sensitization training in Aplysia leads to an increase in the express A;Accession: B44261; MUID:93077669; PMID:1360013

A;Accession: B44261
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-208 <KUH>
A;Note: sequence extracted from NCBI backbone (NCBIP:118950)
C;Genetics:

A;Gene: HSC70 C;Function:

A,Description: involved in protein folding and assembling/disassembling of protein comp. C,Superfamily: heat shock protein 70 C,Keywords: ATP; molecular chaperone

Gaps . 0 Length 208; 1; Indels DB 2; Score 42; Pred. No. 91.3%; 88.9%;

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0; Mismatches Query Match
Best Local Similarity 88.5
Best Local 8; Conservative σ 1 SLFEGIDIY ð

SLFEGIDFY 140

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dnaK-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment) N;Alternate names: 70K heat shock protein C;Species: Oncorhynchus mykiss (rainbow trout) C;Decies: Oncorhynchus mykiss (rainbow trout) C;Dete: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999

C;Accession: II1344
R;Kothary, R.K.; Jones, D.; Candido, E.P.M.
Mol. Cell. Biol. 4, 1785-1791, 1984
A;Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization of c
A;Reference number: I51344; MUID:85036330; PMID:6092938

A;Cross-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804 C;Function: A;Accession: 151344 A;Catus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-278 - KROT-

A;Description: involved in protein folding and assembling/disassembling of protein compl C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone

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R; Borchiellini, C.; Le Parco, Y. submitted to the EMBL Data Library, September 1997
A; Reference number: Z22983
A; Accession: T45476
A; Retarus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-468 < BOR>
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heat-shock protein 70 [imported] - Bunicella cavolini (c)Species: Bunicella cavolini
C)Species: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C)Accession: T45478
R; Borchiellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A; Reference number: Z22983
A; Reference number: Z22983
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 2; Length 467;
Pred. No. 1.3;
0; Mismatches 1; Indels
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R;Borchiellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z22983
A;Accession: T45479
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residuss: 1-467 -46Rx-
A;Cross-references: EMBL:AF026520; PIDN:AAC05364.1
C;Genetics:
A;Genetics:
A
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88.9%; Pred. No. 1.3;
Live 0; Mismatches 1
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A;Molecule type: mRNA
A;Residues: 1-469 <BOR>
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C;Genetics:
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0; Mismatches
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88.9%;
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Best Local Similarity 86...
8, Conservative
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Best Local Similarity 88.5
Matches 8; Conservative
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R;Lowe, D.G.; Moran, D.A.
B;Lowe, D.G.; Moran, D.A.
A;Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000 he
A;Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000 he
A;Reference number: A26283; MUID:86111900; PMID:2868009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. Accession: A26283
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Kesidues: 1-420 < LONA
A. Cross-references: GB: M12571; NID: 9194014; PIDN: AAA57234.1; PID: 9387208
A. Note: the authors translated the codon CTG for residue 173 as Val and CGC for residue C. Function:
A. Moleculon: A. Moleculon: Involved in protein folding and assembling/disassembling of protein comple; Superfamily: heat shock protein 70
C. Superfamily: heat shock protein 70
C. Keywords: ATP; molecular chaperone
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C;Species: Chondrosia reniformis
C;Dacies: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45477
R;Borchiellini, C:; Le Parco, Y
submitted to the EMBL Data Library, September 1997
A;Reference number: 222983
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C;Species: Bunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45479
                                                                                                                                                                                                                                                                                                                                                                                                                             dnaK-type molecular chaperone - mouse (fragment)
NiAlternate names: heat shock protein 68
C.Specias: Mus musculus (house mouse)
C.Specias: Mus musculus (house mouse)
C.Specia: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
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                                             Score 42; DB 2; Length 278;
Pred. No. 0.72;
0; Mismatches 1; Indels
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A,Molecule type: mRNA
A,Residues: 1-467 - EDBJ
A,Cross-references: EMBL:AF026517; PIDN:AAC05362.1
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                                                        91.3%;
                        Query Match
Best Local Similarity 86...
8; Conservative
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Matches 8; Conservative
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Matches 8; Conservative
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T45479
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C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999 C;Accession: A2546 R;Accession: A2546 R;Accession: A2546 R;Mcrimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S. J. Biol. Chem. 261, 12692-12699, 1986 A;Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene A;Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene A;Mcession: A2546 MID:86304452; PMID:3017985 A;Mcession: A2544 CANDA A;Molecule type: DNA A;Molecul
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A;Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
A;Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as V;
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J. Biol. Chem. 268, 23267-23274, 1993
A;Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an
A;Reference number: A48872; MUID:94043116; PMID:8226849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N'Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein ag
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A; Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein A; Reference number: S31766
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A;Molecule type: mRNA
A;Residues: 1-638 «SNA Passinies: 1.738 «SNA Passinies: 1.738 «SNA Passinies: 1.738 «SNA Passinies, 1.7 Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
FEBS Lett. 355, 282-286, 1994
A;Title: The hsc70 gene which is slightly induced by heat is the main virus inducible
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C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
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NyAlternate names: heat shock protein 70
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C;Accession: S31766; 136927
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Pred. No. 1.8;
0; Mismatches
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88.9%; Pred. No. 1.8;
iive 0; Mismatches
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 SLFEGIDFY 288
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: Ā48872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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probable heat shock protein [imported] - Arabidopsis thaliana ("Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Saccession: H96605
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 200
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Razo, M.; Robel P. Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reterence number: A86141; MUID:21016719; PMID:11130712
A; Robel Lype: DNA
A; Reduces: Left < 2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diak-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)
N.Alternate names: heat shock cognate protein 70
N.Alternate names: heat shock cognate protein 70
S.Accession: Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
C.Accession: T45471
S.F.Boves, H.; Mintext, U; Dittrich, W.; Faix, J.; Gerisch, G.
A.Reference number: Z22980
A.Reference number: Z22980
A.Reference number: Z22980
A.Resion: T45471
A.Resion: T45471
A.Residues: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-632 cBOV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:AE005173; NID:g11024845; PIDN:AAG26930.1; GSPDB:GN00141
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Pred. No. 1.8;
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A;Experimental source: strain AX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 2;
Pred. No. 1.7;
0; Mismatches
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A;Note: localized to filopodias and cortex
C;Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dnaK-type molecular chaperone - chicken N;Alternate names: heat shock protein 70 C;Species: Gallus gallus (chicken)
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C; Superfamily: heat shock protein 70
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Best Local Similarity 88.50,
-169 8; Conservative
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Best Local Similarity 88.2
Best Local 8; Conservative
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C; Genetics:

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A; Gene: F13N6

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A, Accession: S64772
A, Molecule type: DNA
A, Residues: 1-639 - GGDF>
A, Coss-references: EMBL: Z73129; NID: g1360201; PIDN: CAA97472.1; PID: g1360202; MIPS: YLLO
A, Experimental source: strain S288C
A, Experimental source: strain S288C
Submitted to the Protein Sequence Database, May 1996
A, Reference number: S64775
A, Accession: S64775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Experimental source: strain 5288C
R.Purnelle, B.; Goffeau, A.
submitted to the EMBL Data Library, April 1996
submitted to the EMBL Data Library, April 1996
mily and a new ABC transporter homologous to the human multidrug resistance protein.
A.Reference number: $69380
A.Accession: $69380A.Accession: $69
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C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
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R;Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.
Gene 64, 241-255, 1988
A;Title: The Caenchabditis elegans hsp70 gene family: a molecular genetic characteriz
A;Reference number: JT0285; MUID:88297155; PMID:2841196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: involved in protein folding and assembling/disassembling of protein com C; Superfamily: heat shock protein 70 C; Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
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NjAlternate names: heat shock protein 70 A
C;Species: Caenorhabditis elegans
C;Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999
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Pred. No. 1.8;
0; Mismatches
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Pred. No. 1.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: MIPS: YLL024c; SGD: S0003947
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 72-639 <DUE>
A;Cross-references: EMEL:Z73129; MIPS:YLL024c
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88.9%;
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A; Introns: 69/1; 331/3; 558/3
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Best Local Similarity
...as 8; Conserve
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                     A,Residues: From RNA
A,Residues: 1-638 <RES-
A,Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
A,Experimental source: kidney; cell line COS-1
C,Genetics: A,Gene: hsp70
C,Function:
A,Description: involved in protein folding and assembling/disassembling of protein compl C,Superfamily: heat shock protein 70
C,Reywords: ATP; molecular chaperone
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Gene 121, 353-358, 1992
A;Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70
A;Reference number: JC1391; MUID:93077053; PMID:1339375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           duak-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)
Alternate names: heat shock protein YG102; protein L0971; protein XL1024c
C;Species: Saccharomyces cerevisiae
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Jun-2000
C;Accession: 820139; 864772; 869383
R;Slater, M.R.; Craig, E.A.
Nucleic Acids Res. 17, 805-806, 1989
A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.
A;Reference number: $20139; MUID:89128457; PMID:2644626
A;Accession: $20139
A;Steus: translation not shown
A;Molecule type: DNA
A;Residues: 1-639 <61AA
A;Residues: 1-630 <61AA
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C;Species: Paracentrotus lividus (common urchin)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
C;Accession: JC1391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X61379, NID:g312916; PIDN:CAA43653.1; PID:g312917
C;Genetics:
A;Gene: hsp70IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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N;Alternate names: heat shock protein 70IV; hsp70IV protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.3%; Score 42; DB 2; Length 639;
Larity 88.9%; Pred. No. 1.8;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 638;
                      A;Reference number: 136927; MUID:95080396; PMID:7988690 A;Accession: 136927
                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 2;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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A; Residues: 1-639 <SCO>
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Best Local Similarity
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C; Function:
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Sequence 13352, A Sequence 12954, A Sequence 12954, A Sequence 24597, Sequence 8613, Ap Sequence 47005, A Sequence 2025, Ap Sequence 2016, Ap Sequence 2106, Ap Sequence 2409, Ap Sequence 22, Applisequence 621, App Sequence 622, 
                                                                                                                                                                              September 15, 2004, 10:34:32; Search time 40.7368 Seconds (without alignments) 29.609 Million cell updates/sec
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1: /cgn2 6/ptodata/2/paa/PCT NEW COMB.pep:*

2: /cgn2 6/ptodata/2/paa/US06_NEW COMB.pep:*

3: /cgn2 6/ptodata/2/paa/US08_NEW-COMB.pep:*

5: /cgn2 6/ptodata/2/paa/US08_NEW-COMB.pep:*

6: /cgn2 6/ptodata/2/paa/US08_NEW-COMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-60-565-632-12954

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US-60-581-351-2025

US-60-581-351-2025

US-60-581-351-2016

US-60-581-351-2016

US-60-581-351-2016

US-60-581-351-2016

US-60-581-351-2016

US-60-581-326-8611

US-60-581-326-8611

US-60-581-326-8611

US-60-581-326-8611

US-60-581-326-8611

US-60-566-425-621

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US-60-570-505-54
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Sequence Sequence Sequence Sequence

Sequence 497, App Sequence 27, Appl Sequence 28, Appl Sequence 30, Appl Sequence 30, Appl Sequence 653, App Sequence 655, App Sequence 657, Appl Sequence 41, Appl Sequence 146, Appl Sequence 146, Appl Sequence 146, Appl Sequence 2015, Appl Sequence 2019, Appl Sequen		Other Molecules Associated With or Plant Improvement 507_1.pep	Length 181; ; Indels 0; Gaps 0;	Shock A Discrete Domain and is
1 7 US-60-570-505-497 1 7 US-60-576-801-28 1 7 US-60-576-801-29 1 7 US-60-576-801-29 1 7 US-60-576-801-403 1 7 US-60-576-812-655 1 7 US-60-576-812-655 1 7 US-60-576-812-655 1 7 US-60-576-812-655 1 7 US-60-576-812-657 1 7 US-60-592-191-42 1 7 US-60-592-191-42 1 7 US-60-592-191-42 1 7 US-60-592-191-43 1 7 US-60-592-191-44 2 US-60-592-191-44 3 US-60-592-191-44 5 US-10-885-523-10 6 US-10-885-523-10 7 US-60-581-351-2015 7 US-60-581-351-2015	ALIGNMENTS	ss and reof Fc L	3%; Score 42; DB 6; 3%; Pred. No. 1.3; 0; Mismatches 1	3 icitation By Heat n Proteins Maps To dependent 885,523 1,534
27 28 29 29 30 31 31 32 32 33 34 42 91 33 34 42 91 33 42 91 33 42 91 34 42 91 35 42 91 37 42 91 37 42 91 37 42 91 33 42 91 33 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 33 44 42 91 34 44 42 91 34 44 42 91 34 44 42 91 34 44 44 44 44 44 44 44 44 44		RESULT 1  US-10-767-701-33352  Sequence 33352, Application US/10767701  GENERAL INFORMATION: APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecule TITLE OF INVENTION: Plants and Uses Then TITLE OF INVENTION: Plants and Uses Then TITLE OF ENVENTION: Plants and Uses Then CURRENT APPLICANTION NUMBER: US/10/767,700; NUMBER OF SEQ ID NOS: 63128  SEQ ID NO 33352 LENGTH: 181 TYPE: PRT ORGANISM: Sorghum bicolor FEATURE: ORGANISM: Clone ID: SORBI-28MANUS-10-767-701-33352	Ouery Match Best Local Similarity 88 Matches 8, Conservative Oy 1 SLFEGIDIY 9	WESULT 2  1. Sequence 12, Application US/1088552; 1. GENERAL INFORMATION: 1. APPLICANT: Huang, Oian 1. APPLICANT: Richmond, Joan F.L. 1. APPLICANT: Cho, Bryan K. 1. APPLICANT: Cho, Bryan K. 1. APPLICANT: Cho, Jiaczhu 1. APPLICANT: Chen, Jiaczhu 1. APPLICANT: Chen, Jiaczhu 1. APPLICANT: Biesn, Herman N. 1. TITLE OF INVENTION: In Vivo CTL BI: 1. TITLE OF INVENTION: CD4+T Cell-Ing; 1. TITLE OF INVENTION: DATE: 2004-07-01; 1. PRIOR APPLICATION NUMBER: US/09/76; 1. PRIOR FILING DATE: 2001-01-16

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APPLICANT: Baum, James A
APPLICANT: Rovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Zhang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants an TITLE OP INVENTION: Compositions Thereof
FILE REFERENCE: 38-21(53403)B
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
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US-10-425-115-345997
Squence 345997, Application US/10425115
SGUENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 345997
LENGTH: 296
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LOCATION: (1)..(296)
LOCATION: (1)..(206)
FEATURE INFORMATION: unsure at all Xaa locations
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Pred. No. 2.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                        Score 42; DB Pred. No. 2; 0; Mismatches
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: Patentin version 3.2
SEQ ID NO 12954
LENGTH: 263
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US-60-579-062-12954
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
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APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maolong
APPLICANT: Lu, Maolong
APPLICANT: Munylkwa, Tichifa R. I.
APPLICANT: Wu, wei
APPLICANT: Wu, wei
APPLICANT: Wu, wei
APPLICANT: Mu, wei
APPLICANT: Annay Beal
APPLICANT: Annay Bain
APPLICANT: Mu, wei
APPLICANT: Compositions thereof
TITLE OF INVENTION: Compositions thereof
FILE REFERENCE: 38-21 (53403) C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MULYLWA, Tichifa R. I.
APPLICANT: Muly Wei
APPLICANT: Characteristic Repetits of the second of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 6; Length 209;
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                           FEATURE:
, OTHER INFORMATION: Murine hsp70 - Segment II US-10-885-523-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
            PRIOR APPLICATION NUMBER: PCT/US00/32831
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PASLERQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-60-565-632-12954
; Sequence 12954, Application US/60565632
; GENERAL INFORMATION:
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Rovalic, David K.
Larosa, Thomas J.
Lu, Maolongman Tichifa R. I.
Roberts, James K.
Wu, Wei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ), ORGANISM: Diabrotica virgifera
US-60-565-632-12954
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88.9%;
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Best Local Similarity 88.9%;
Matches 8; Conservative (
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Best Local Similarity 88.9
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                                                                                                                                                                                                                                                                                                  ORGANISM: Unknown
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US-60-579-062-12954
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LENGTH: 263
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APPLICANT:
APPLICANT:
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us-09-673-795-1.rapn

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APPLICANT: Baum, James A

APPLICANT: Kovalic, David K.

APPLICANT: Monoral Thomas J.

APPLICANT: Larosa, Thomas J.

APPLICANT: Larosa, Thomas J.

APPLICANT: Larosa, Tichifa R. I.

APPLICANT: Munylkwa, Tichifa R. I.

APPLICANT: Wu, Wai,

APPLICANT: Roberts, James K.

APPLICANT: Roberts, James K.

APPLICANT: Cannopaition Thereof

TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and

TITLE OF INVENTION: Compositions Thereof

TITLE OF INVENTION: Compositions Thereof

TITLE OF INVENTION: Compositions Thereof

TITLE OF INVENTION: UNMBER: US/60/565,632

CURRENT APPLICATION NUMBER: US/60/565,632

NUMBER OF SEQ ID NOS: 15449

SOFTWARE: Patentin version 3.2

SEQ ID NO 8611

LENGTH: 639
                                                                                                                                       Sequence 47005, Application US/10767701

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants us/10/767,701

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT PILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

LENGTH: 601
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NAME/KEY: misc feature

LOCATION: (69)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-565-632-8611
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US-10-767-701-47005
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Pred. No. 4.8;
0; Mismatches
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OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 8611, Application US/60565632
; GENERAL INFORMATION:
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ORGANISM: Diabrotica virgifera
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ORGANISM: Sorghum bicolor
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Matches 8; Conservative
                                                       154 SLFEGIÖFY 162
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NAME/KEY: misc feature
LOCATION: (56)...(56)
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OTHER INFORMATION: Xaa
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NAME/KEY: unsure
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APPLICANT: Wh, Wei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions thereof
TITLE OF INVENTION: Compositions thereof
TITLE REFERENCE: 38-21 (53403) C
CURRENT APPLICATION NUMBER: US/66/579,062
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: Patentin version 3.2
TENCOME. 100 8613
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REPRENCE: 38-21(53372)B
GURRENT APPLICATION WUMBER: US/60/581,351
CURRENT APPLICATION WUMBER: US 60/479,962
PRIOR APPLICATION WUMBER: US 60/479,962
PRIOR APPLICATION WUMBER: US 60/479,962
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: Patentin version 3.2
INDICTH: 503
TYPE: PRT
TYPE: PRT
TYPE: PRT
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TYPE: PRT
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Pred. No. 4;
0; Mismatches 1; Indels
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Pred. No. 2.9;
0; Mismatches
                                                                                                                                                     ularity 88.9%; Score 42; DB 88.9%; Pred. No. 2.9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8613, Application US/60579062; GENERAL INFORMATION:
APPLICANT: Baum, James A
APPLICANT: Kovalic, David K
APPLICANT: Larcea, Thomas J
APPLICANT: Lu, Maclong;
APPLICANT: Lu, Maclong;
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
                                                                                    ) ORGANISM: Diabrotica virgifera
US-60-565-632-8613
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8613
LENGTH: 376
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US-60-579-062-8613
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Best Local Similarity 88.39,
'-hes 8; Conservative
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Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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US-60-581-351-2025
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APPLICANT:
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APPLICANT:
                                         LENGTH: 37
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PAPELICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINAS
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
FILE REFREENCE: DO1895 PCT
CURRENT PAPELICATION NUMBER: US/10/501,035
CURRENT FILING DATE: 2004-07-09
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SOFTWARE: PATCHING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SSOFTWARE: PATCHING DATE: 2002-01-18
SOFTWARE: PATCHING DATE: 2002-01-18
SOFTWARE: PATCHING DATE: 2002-01-18
SOFTWARE: PATCHING DATE: 2002-01-18
SOFTWARE: ACTIVITY OF SEQ ID NOS: 795
LENGTH: 640
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Sequence 2409, Application US/09949003C
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC
TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF
FILE REPERRENCE: CLOO0791
CURRENT APPLICATION NUMBER: uS/09/949, 003C
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,446
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 74065
SOFTWARE: Patentin version 3.2
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Pred. No.
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GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
                                                                                                                                             US-10-501-035-326; Sequence 326, Application US/10501035; GENERAL INFORMATION:
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                          283 SLFEGIDFY 291
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CRGANISM: Homo sapiens
US-10-501-035-326
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                 1 SLFEGIDIY 9
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Best Local Similarity
Matches 8; Conserv
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US-10-821-234-1519
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LENGTH: 641
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APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Wu, Wei
APPLICANT: Zhang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions thereof
FILE REPERENCE: 38-21 (53403) C
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT PILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 414445
SOFTWARE: Patentin version 3.2
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Sequence 2016. Application US/60581351

GENERAL INFORMATION:
APPLICANT: Laurie, Cathy C
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REFERENCE: 38-21(53372)B
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2003-06-19
FRIOR APPLICATION NUMBER: 05 60/479,962
FRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13380
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2016
ILENGTH: 639
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; LCCATION: (69)..(69)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-579-062-8611
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OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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Pred. No. 5.2;
0; Mismatches 1; Indels
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5.2;
  DB 7; Length 639;
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91.3%; Score 42; DB 7
88.9%; Pred. No. 5.2;
Live 0; Mismatches
                                                                                                                                                                                                                                     Sequence 8611, Application US/60579062
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               APPLICANT: Baum, James A
APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maclong
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
APPLICANT: Wu, Wei
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Best Local Similarity 88.5.
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US-60-579-062-8611
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LENGTH: 639
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FILE REFERENCE: 821A

CURRENT APPLICATION: Methods for Diagnosis and Treatment of Preeclampsia

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR PLING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PL SEQ_Genes Version 1.0

LENGTH: 641

TYPE: PRT

CORGANISM: Homo sapiens

US-10-821-234-1519

Query Match

Best Local Similarity 88.9%; Pred. No. 5.2;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CV 1 SLFEGIDIY 9

Db 286 SLFEGIDFY 294

Search completed: September 15, 2004, 10:48:20
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GENERAL INFORMATION:
APPLICANT: Wang, Rong-fu
TITLE OF INVENTION: Matent Fibronectin and Tumor Metastasis
FILE REFERENCE: HO-P02464W00
CURRENT APPLICATION NUMBER: PCT/US03/16736
CURRENT APPLICATION NUMBER: PC/03-05-28
PRIOR FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.1
SEQ ID NO 117
FIRING PATENTIN PATENT OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46; DB 1; Length 9;
Pred. No. 5.5e+06;
           US-10-673-795-1

US-10-673-795-1

US-10-110-731-1

US-10-673-795-2

US-10-673-795-2

US-10-110-731-2

US-09-673-795-8

US-09-673-795-8

US-09-673-795-8

US-09-673-795-8

US-09-673-795-8

US-09-791-57-3064

US-09-791-57-3064

US-09-791-57-15866

US-09-791-57-15866

US-09-791-57-15866

US-10-328-953-319

US-10-328-953-319

US-10-328-953-328

US-10-328-953-330

US-09-791-537-76316

US-09-791-537-76318

US-09-791-537-76318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic Peptide PCT-US03-16736-117
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Best Local Similarity
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TYPE: PRT
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                                                                                                               September 15, 2004, 10:34:17; Search time 281.368 Seconds (without alignments)
31.221 Million cell updates/sec
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18: /cgn2
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 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Result No. ö

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US-051-795-2
; Sequence 2, Application US/09673795
; Sequence 2, Application US/09673795
; GENERAL INFORMATION:
; APPLICANT: TRIBBEL, FREDERIC
; APPLICANT: GAUDIN, CATHERINE
; TITLE OF INVENTION: MUTATED PEPTIDE COMPOUNDS, DERIVED FROM hsp70, USEFUL IN CANCER
; TITLE OF INVENTION: IMMUNOTHERAPY
; TITLE OF INVENTION: UMMUNOTHERAPY
; FILE REFREENCE: 03715.0069
; CURRENT APPLICATION NUMBER: US/09/673,795
; CURRENT FILING DATE: 2000-10-20,
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TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis FILE REFERENCE: HO-P02484US1
CURRENT APPLICATION NUMBER: 0210/447,161
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/383,530
PRIOR FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 148
SOFTWARE: Patentin version 3.1
SEQ ID NO 117
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ilarity 100.0%; Pred. No. 5.5e+06;
Conservative 0; Mismatches
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TITLE OF INVENTION: THEIR USE IN THERAPEUTICS
CURRENT APPLICATION NUMBER: US/10/110,731
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: EP 99 120 484.3
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 10
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PRIOR APPLICATION NUMBER: PCT/FR99/00957
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1998-04-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Vers. 2.1
SEQ ID NO 2
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic Peptide US-10-447-161-117
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                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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; Sequence 1, Application US/09673795
; Sequence 1, Application US/09673795
; GENERAL INFORMATION:
APPLICANT: TRIEBEL, FREDERIC
; APPLICANT: GAUDIN, CATHERINE
; TITLE OF INVENTION: MUTATED PEPTIDE COMPOUNDS, DERIVED FROM hsp70, USEFUL IN CANCER;
; TILLE OF INVENTION: MUTATED PEPTIDE
; TILLE OF INVENTION: MUTATED PEPTIDE
; TILLE OF INVENTION: MUTATED PEPTIDE
; FILLE REFERENCE: 03715.006
; CURRENT APPLICATION NUMBER: PCT/FR99/00957
; PRIOR APPLICATION NUMBER: FR 98 05033
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: FR 98 05033
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Vers. 2.1
; SEQ ID NO 1
; FILLE OF INVENTION OF SECOND SECO
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TITLE OF INVENTION: NEW LYMPHOCYTES, A PROCESS FOR PREPARING THE SAME AND
TITLE OF INVENTION: THEIR USE IN THERAPEUTICS
FILE REFERENCE: WE BA IDM STRE
CURRENT APPLICATION NUMBER: US 102-04-15
PRIOR PILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PAUGHTIN VETSION 3.1
LENGTH: 9
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APPLICANT: Wang, Rong-fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10110731 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 9; Conservative 0;
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                                  Conservative
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CRGANISM: Homo sapiens
US-10-110-731-1
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CORGANISM: Homo sapiens
US-09-673-795-1
                                                                                               1 SLFEGIDIY 9
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                                      9;
                                                                                                                                                                                                                                                    RESULT 2
US-09-673-795-1
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                                      Matches
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Sequence 203858, Application US/10424599
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE SPERENTENT: 32163233B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ELENGTH: 130
                                                                                                                                Gequence 3, Application US/10110731
GENERAL INFORMATION:
APPLICANT 1.D.M. IMMUNO-DESIGNED MOLECULES
APPLICANT: I.D.M. IMMUNO-DESIGNED MOLECULES
TITLE OF INVENTION: NEW LYMPHOCYTES, A PROCESS FOR PREPARING THE SAME AND
FILE REPRENCE: WOB 99 BA 1DM STRE
CURRENT APPLICATION NUMBER: US/10/110,731
PRIOR PILING DATE: 2002-04-15
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PALCHIN VETSION 3.1
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88.9%; Pred. No. 5.5;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 27; Length 10;
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LOCATION: (1)..(130)
OTHER INFORMATION: unsure at all Xaa locations
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Pred. No. 0.29
0; Mismatches
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ORGANISM: Homo sapiens
                1 SLFEGIDFY 9
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Matches 8; Conserv
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Matches 8; Conserv
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US-10-424-599-255293
                                                                                            RESULT 9
US-10-110-731-3
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### APPLICANT: TRIEBEL, FREDERIC

### APPLICANT: GAUDIN, CATHERINE

### TITLE OF INVENTION: IMMUNOTHERAPY

### TITLE OF INVENTION: MUNDERRAPY

### FILE REFERENCE: 03715.0069

### CURRENT APPLICATION NUMBER: US/09/673,795

### CURRENT PILING DATE: 2000-10-20

### PRIOR APPLICATION NUMBER: PR 98 05033

### PRIOR FILING DATE: 1999-04-22

### PRIOR PLING DATE: 1999-04-22

### PRIOR PLING DATE: 1999-04-22

### NUMBER OF SEQ ID NOS: 8

### SOFTWARE: Patentin Vers. 2.1

### SOFTWARE: Patentin Vers. 2.1
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APPLICANT: TRIBBEL, FREDERIC
APPLICANT: GAUDIN, CATHERINE
TITLE OF INVENTION: MUTATED PRPTIDE COMPOUNDS, DERIVED FROM hsp70, USBFUL IN CANCER
TITLE OF INVENTION: INMUNOTHERAPY
FILE REPERBNCE: 03715.0069
CURRENT APPLICATION NUMBER: 18/09/673,795
CURRENT PILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
RIOR FILING DATE: 1998-04-22
ROBER OF SEQ ID NOS: 8
SOFTWARE: PATCHIN VETS: 2.1
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                                                                                    100.0%; Score 46; DB 27; Length 10; 100.0%; Pred. No. 0.045; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20; Length 10;
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Pred. No. 5.5e+06;
0; Mismatches 1;
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Pred. No. 0.29;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09673795 GENERAL INFORMATION:
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88.9%;
                                                                           Query Match
Best Local Similarity 100.
Matches 9, Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Homo sapiens
US-09-673-795-8
                                                                                                                                                                 1 SLFEGIDIY 9
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; ORGANISM: Homo sapiens
US-09-673-795-7
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Best Local Similarity
Matches 8; Conserva
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Matches 8; Conserv
                         ; ORGANISM: DS-10-110-731-2
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APPLICANT: Huang, Qian
APPLICANT: Huang, Qian
APPLICANT: Richmond, Joan F.L.
APPLICANT: Richmond, Joan F.L.
APPLICANT: Richmond, Joan F.L.
APPLICANT: Richmond, Joan F.L.
APPLICANT: Palliser, Deborah
APPLICANT: Chen, Jianzhu
APPLICANT: Eisen, Herman N.
APPLICANT: Young, Richard A.
ITILE OF INVENTION: Drotein Fusion Proteins Maps To A Discrete Domain and is
TITLE OF INVENTION: Drotein Fusion Proteins Maps To A Discrete Domain and is
TITLE OF INVENTION: CD4+T Cell-Independent
FILE REFERENCE: 0399.2006-003
CURRENT APLICATION NUMBER: US/09/761,534A
CURRENT FILING DATE: 2001-01-16
PRIOR PELING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/USO0/32831
PRIOR PILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FREESEQ for Windows Version 4.0
SSG ID NO 12
LENGTH: 209
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Sequence 225.

GENERAL INFORMATION:

GENERAL SEQUENCE 225.

GENERAL SEQUENCE SEQUENCE:

TITLE OF INVENTION:

TITLE OF IN
                                                                                           Length 208;
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                                                                                              DB 22;
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Pred. No. 9.7;
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                                                                                           Score 42; DB 2
Pred. No. 9.5;
0; Mismatches
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US-09-761-534A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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88.9%;
                                                                                           91.3%;
88.9%;
; ORGANISM: Aplysia californica
US-09-791-537-3064
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Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                 Query Match
Best Local Similarity 88.5
Matches 8; Conservative
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Best Local Similarity
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ORGANISM: Unknown
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US-60-196-712-2253
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APPLICANT: Bionomix, Inc.

APPLICANT: Bionomix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Debe, Oseeph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001.02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

SEQ ID NO 3064

LENGTH: 208

TYPE: PRT
                                   APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B CURRENT APPLICATION NUMBER: US/10/424,599

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 255293

LENGTH: 174
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Sequence 2.2471, Application US/09417507

GENERAL INFORMATION:
APPLICANT: KEITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: FUNGATUS FOR DIAGNOSTICS AND THERAPBUTICS
FILE REPERENCE: PATH99-10

CURRENT APPLICATION NUMBER: US/09/417,507

CURRENT PILING DATE: 1999-10-14

NUMBER OF SEQ ID NOS: 44312

SEQ ID NO 2.2471

LENGTH: 175
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Pred. No. 7.8;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(174)
OTHER INFORMATION: unsure at all Xaa locations
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3064, Application US/09791537; GENERAL INFORMATION:
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88.9%;
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Best Local Similarity 88.2
Best Local Similarity 88.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.9:
                      Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 SLFEGIDFY 47
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CORGANISM: A.fumigatus
US-09-417-507-22471
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                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-424-599-255293
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US-09-417-507-22471
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0; Gaps

0; Mismatches 1; Indels 8; Conservative Matches

1 SLFEGIDIY 9 ||||||| | 199 SLFEGIDFY 207

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September 15, 2004, 10:35:52; Search time 81 Seconds (without alignments) 35.632 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/NSO6_NEW PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1335176 seqs, 320689617 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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46
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	was 11 aprendition	Semience 203858	Secritor 200000	Segment 33350	Semience 12 Anni	Semience 1 Appli	Semience 763 ann	Semience 319 and	Semience 326 Ann	Semience 323, App	Semience 328 App	Segmence 320, App	Semience 329, App	Semience 3466 An	Sequence 12366. A	
SUMMARIES	QI	US-10-447-161-117	US-10-424-599-203858	US-10-424-599-255293	US-10-767-701-33352	US-09-761-534A-12	US-10-328-953-1	US-10-408-765A-763	US-10-328-953-319	US-10-328-953-326	US-10-328-953-327	US-10-328-953-328	US-10-328-953-329	US-10-328-953-330	US-10-108-260A-3466	US-10-369-493-12366	
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	Query Match Length DB	σı	130	174	181	209	377	380	381	392	393	393	393	405	476	516	
%	Match	100.0	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	
	Score	46	42	42	42	42	42	42	42	42	42	42	42	42	42	42	
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Semience 47005	Semience 2 Appli	Semience 22298 A	Segmence 6233 Ap	Segmence 255 App	Segment & apracas	Semience 1 Appli	Semience 146 Ann	Sequence 5. Appli	Sequence 28. April	Semence 97 Appl	Sequence 10. Appl	Sequence 1394. An	Sequence 1760. An	Semience 146. Ann	2277	edience	62493	Semience 62884. A	4146. 4	Sequence 193936	-	Sequence 204. App	õ	Ö	Semience 724 Ann	727 0	Semience 242 Ann	Semience 4304 an	Sequence 46700, A
US-10-767-701-47005	US-10-132-556A-2	US-10-369-493-22298	US-10-369-493-6233	US-10-408-765A-255	l	US-09-935-642-1	US-09-919-039-146	US-10-380-408A-5	US-10-316-253-28	US-10-316-253-97	US-09-761-534A-10	US-10-369-493-1394	US-10-369-493-1760	US-10-451-467A-146	US-10-369-493-22772	US-10-425-114-62894	US-10-425-114-62493	US-10-425-114-62884	US-10-369-493-4146	US-10-437-963-193936	US-09-733-179A-11	US-09-919-039-204	US-10-755-889-396	US-10-437-963-193938	US-09-925-302-724	US-09-925-302-724		13.	US-10-767-701-46700
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91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91,3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91,3	89.1	89.1	89.1	89.1	89.1	89.1	89.1	84.8	84.8	84.8
42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	41	41	41	41	41	41	41	ი ო	39	39
16	17	18	19	20	21	22	23	24	25	26	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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WS-10-447-161-117

WS-10-447-161-117

WS-10-447-161-117

Sequence 117, Application US/10447161

Publication No. US20040023314A1

SERNEAL INFORMATION: Mutant Fibronectin and Tumor Metastasis

TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis

CURRENT APPLICATION NUMBER: US/10/447,161

CURRENT PILING DATE: 2002-05-28

PRIOR APPLICATION NUMBER: 60/383,530

PRIOR APPLICATION NUMBER: 60/383,530

PRIOR APPLICATION NUMBER: 60/383,530

NUMBER OF SEQ ID NOS: 148

SOFTWARE: Patentin version 3.1

LENGTH: 9

CORFANISM: Artificial Sequence

FRATURE: OTHER INFORMATION: Synthetic Peptide

US-10-447-161-117

Query Match

Best Local Similarity 100.0%; Score 46; DB 16; Length 9;

Matches 9; CONSERVATIVE 0; Mismatches 0; Indels 0; Gaps

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1 SLFEGIDIY 9

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Db 1 SLFEGIDIY 9

RESULT 2
US-10-424-599-203858
; Sequence 203858, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

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FEATURE:

Matches

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| Patent NO. USJULINIAGE AND |
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Huang, Qian |
| APPLICANT: Richmond, Joan F.L. |
| APPLICANT: Che, Bryan K. |
| APPLICANT: Che, Jianzhu |
| APPLICANT: Chen, Jianzhu |
| APPLICANT: Poung, Richard A. |
| TITLE OF INVENTION: IN Vivo CTL Elicitation By Heat Shock |
| TITLE OF INVENTION: CD4+T Cell-Independent |
| TITLE OF INVENTION UNMERR: US/09/761,534A |
| CURRENT FILING DATE: 2000-10-1-16 |
| PRIOR FILING DATE: 2000-11-4 |
| NUMBER OF SEQ ID NOS: 25 |
| SOFTWARE: FastSEQ for Windows Version 4.0
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement File Reference: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 SEQ ID NO 33352 LENGTH: 181
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Publication No. US20040071656A1;
GENERAL INFORMATION:
APPLICANT: Wieland, Felix
APPLICANT: Hartl, Franz-Ulrich
TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies;
FILE REFERENCE: 11390/46101
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                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: CLONE ID: SORBI-28MAY03-C30507_1.pep
US-10-767-701-33352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.3%; Score 42; DB 9;
88.9%; Pred. No. 2.5;
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US-09-761-534A-12
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; Sequence 12, Application US/09761534A
; Patent No. US20020146426A1
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                                                                                                                                                                                                                                                                                                                                                               Query Match 91.3
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Sorghum bicolor
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Best Local Similarity
Matches 8; Conserv
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ORGANISM: Unknown
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US-10-328-953-1
                                                                                                                                                                                                                                                                      FEATURE
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Sequence 255293, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Covalic David K

APPLICANT: APPLICANT: Covalic David K

APPLICANT: APPLICANT: And Vihua

APPLICANT: APPLICANT: Covalic David K

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5322)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 255293

LENGTH: 174

FILE DENGTH: 174
                              APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38 - 21 (53233) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 203858
LENGTH: 130
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Pred. No. 1.5;
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US-10-424-599-255293
                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Clone ID: PAT_MRT3847_26109C.1.pep US-10-424-599-203858
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OTHER INFORMATION: unsure at all Xaa locations FEATURE:
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: (1)..(130)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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; Publication No. US20040172684A1
; GENERAL INFORMATION:
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SLFEGIDIY 9
                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
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US-10-767-701-33352
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; OTHER INFORMATION: fusion polypeptide: hsp70(1-381)-Gly-Ser-Gly-gp100(209-217:Met210
US-10-328-953-326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wieland, Felix
APPLICANT: Wieland, Felix
APPLICANT: Hartl, Franz-Ulrich
TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
FILE REFERENCE: 11390/46101
CURRENT APPLICATION NUMBER: US/10/328,953
CURRENT PILING DATE: 2002-12-23
FRIOR APPLICATION NUMBER: US 60/342,570
PRIOR PILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-29
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-09-28
PRIOR FILING DATE: 2002-09-28
NUMBER OF SEQ ID NOS: 331
SEQ ID NO 326
LENGTHE: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATABASE ACCESSION NUMBER: Genbank GI:15277246; amino acids 1-381 of hsp70; DATABASE ENTRY DATE: 2001-08-22
US-10-328-953-319
                           TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 12;
Pred. No. 5.1;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.9;
0; Mismatches
                                          FILE REFERENCE: 11390/46101
CURRENT APPLICATION NUMBER: US/10/328,953
CURRENT APPLICATION NUMBER: US/10/328,953
CURRENT APPLICATION NUMBER: US 60/342,570
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 60/343,884
PRIOR FILING DATE: 2001-12-28
PRIOR FILING DATE: 2001-12-8
PRIOR APPLICATION NUMBER: US 60/312,620
PRIOR APPLICATION NUMBER: US 60/399,342
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 60/399,342
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-09-28
NUMBER OF SEQ ID NOS: 331
SOFTWARE: WORDPERFECT 8:0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.3%; Score 42;
88.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 326, Application US/10328953
Publication No. US20040071656A1
GENERAL INFORMATION:
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 ŚLFEGIDFY 294
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Best Local Similarity
Matches 8; Conserv
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LENGTH: 381
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank GI:15277246; amino acids 5-381 of hsp70
DATABASE ENTRY DATE: 2001-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
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APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gaven W.
APPLICANT: Glenn, Gavy M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DEBNIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPREBLICE 660088.465
CURRENT APPLICATION NUMBER US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE FALSEO for Windows Version 4.0
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Pred. No. 4.9;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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CURRENT APPLICATION NUMBER: US/10/328,953
CURRENT FILING DATE: 2002-12-23
FRIOR APPLICATION WUMBER: US 60/342,570
FRIOR PLILNG DATE: 2001-12-26
FRIOR PLILNG DATE: 2001-12-26
FRIOR FILING DATE: 2001-12-28
FRIOR FILING DATE: 2002-0399,342
FRIOR PELING DATE: 2002-04-12
FRIOR APPLICATION NUMBER: US 60/372,620
FRIOR APPLICATION NUMBER: US 60/399,342
FRIOR APPLICATION NUMBER: US 60/399,342
FRIOR APPLICATION NUMBER: US 60/414,834
FRIOR FILING DATE: 2002-07-29
FRIOR PILING DATE: 2002-09-28
NUMBER OF SEQ ID NOS: 331
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO: LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 763, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-10-328-953-319
Sequence 319, Application US/10328953
Publication No. US20040071656A1
GENERAL INPORMATION:
APPLICANT: Wieland, Felix
APPLICANT: Hartl, Franz-Ulrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.3%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Boin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Wannock, Dale E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.3%;
88.9%;
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Best Local Similarity 88.9
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Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLFEGIDFY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 SLFEGIDFY 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRGANISM: Homo sapiens
US-10-408-765A-763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SLFEGIDIY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-10-408-765A-763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-328-953-1
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Wieland, Felix
APPLICANT: Wieland, Felix
TITLE OF INVENTION:
FILE REFERENCE: 11390/46101
CURRENT APPLICANTION WORDER: US/10/328,953
CURRENT APPLICANTION WHRER: US/10/328,953
CURRENT FILING DATE: 2002-12-23
FRIOR APPLICATION WHRER: US 60/342,570
PRIOR APPLICATION WHRER: US 60/342,894
FRIOR PILING DATE: 2001-12-26
FRIOR PELING DATE: 2001-12-28
FRIOR PRILING DATE: 2001-02-38
FRIOR FILING DATE: 2001-02-38
FRIOR FILING DATE: 2002-04-12
FRIOR APPLICATION NUMBER: US 60/372,620
FRIOR APPLICATION NUMBER: US 60/372,620
FRIOR FILING DATE: 2002-04-12
FRIOR FILING DATE: 2002-04-12
FRIOR FILING DATE: 2002-04-29
FRIOR FILING DATE: 2002-03-39
FRIOR FILING DATE: 2002-03-39
FRIOR FILING DATE: 2002-03-31
FRIOR FILING DATE: 2003-09-38
NUMBER OF SEQ ID NOS: 331
                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-10-328-953-329

is equence 329, Application US/10328953

is equence 329, Application WS/10328953

is publication No. US20040071656A1

is debergated in No. US20040071656A1

is debergated in No. US20040071656A1

is debelgant: William Selix

APPLICANT: William Selix

APPLICANT: Wodulation of Heat-Shock-Protein-Based Immunotherapies

is TILE REPERBENCE: 1330/46410

CURRENT FILING DATE: 2002-12-23

PRIOR FILING DATE: 2001-12-28

PRIOR PLICATION NUMBER: US 60/342,570

PRIOR PLICATION NUMBER: US 60/342,570

PRIOR PLICATION NUMBER: US 60/343,884

PRIOR PLICATION NUMBER: US 60/343,884

PRIOR PLICATION NUMBER: US 60/372,620

PRIOR PLILING DATE: 2002-04-12

PRIOR PLILING DATE: 2002-04-22

PRIOR PLILING DATE: 2002-09-28

NUMBER OF SEQ ID NOS: 331

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 329

LENGTH: 393
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OTHER INFORMATION: tyrosinase(368-376:Asp370)-Gly-Ser-Gly-hsp70(1-381)
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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88.9%; Pred. No. 5.1;
91.3%; Score 42; DB 12; Length 393; 88.9%; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Publication No. US20040071656A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 91.3
Best Local Similarity 88.9
Matches 8; Conservative
            Query Match 91.3
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                     286 SLFEGIDFY 294
                                                                                                                                                                       1 SLFEGIDIY 9
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OTHER INFORMATION: fusion polypeptide: gp100(209-217:Met210)-Gly-Ser-Gly-hsp70(1-381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ## Sequence 328, Application US/10328953

## Sequence 328, Application US/10328953

## Sequence 328, Application US/2040071656A1

## Sequence 328, Application No. US20040071656A1

## PEDICANT: Wieland, Felix

## APPLICANT: Wieland, Felix

## APPLICANT: Wieland, Felix

## TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies

## TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies

## TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies

## TITLE OF INVENTION: Worder: US/10/328,953

## CURRENT PILING DATE: 2002-12-23

## PRIOR PELICATION NUMBER: US 60/342,570

## PRIOR PELICATION NUMBER: US 60/343,884

## PRIOR PELICATION NUMBER: US 60/343,884

## PRIOR PILING DATE: 2002-04-12

## PRIOR APPLICATION NUMBER: US 60/399,342

## PRIOR APPLICATION NUMBER: US 60/399,342

## PRIOR PILING DATE: 2002-04-12

## PRIOR PILING DATE: 2002-04-12

## PRIOR PILING DATE: 2002-04-12

## PRIOR PILING DATE: 2002-05-28

## NUMBER: OF SEQ ID NOS: 331

## PRIOR PILING DATE: 2002-09-28

## NUMBER: WordPerfect 8.0 for Windows

## SEQ ID NO 328

## DENGTH: 393

## PRIOR PILING DATE: 2002-09-28

## PRIOR PILIN
                                                                                                                                                                                                                                                     GRINEMAL INVEXMENTION:
GRINEMAL INVEXMENTION:
APPLICANT: Wieland, Felix
APPLICANT: Wieland, Felix
APPLICANT: Hartl, Franz-Ulrich
TITES OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
FILE REFERENCE: 11390/46101
CURRENT APPLICATION NUMBER: US/10/328,953
CURRENT FILING DATE: 2002-12-23
FRIOR APPLICATION NUMBER: US 60/342,570
FRIOR PILING DATE: 2001-12-26
FRIOR APPLICATION NUMBER: US 60/343,884
FRIOR APPLICATION NUMBER: US 60/343,884
FRIOR APPLICATION NUMBER: US 60/372,620
FRIOR APPLICATION NUMBER: US 60/399,342
FRIOR APPLICATION NUMBER: US 60/399,342
FRIOR APPLICATION NUMBER: US 60/414,834
FRIOR FILING DATE: 2002-09-28
NUMBER OF SEQ ID NOS: 331
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 327
LENGTH: 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 91.3%; Score 42; DB 12; Length 393; Best Local Similarity 88.9%; Pred. No. 5.1; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                               Sequence 327, Application US/10328953 Publication No. US20040071656A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 SLFEGIDFY 306
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US-10-328-953-328
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Sequence 12366, Application US/10369493

Sequence 12366, Application US/10369493

Publication No. US20030233675A1

GENERAL INPORMATION:

APPLICANT: Galdwan, Barer, Steven C.

APPLICANT: Glater, Steven C.

APPLICANT: Grater, Steven C.

APPLICANT: Glater, Steven C.

APPLICANT: Grater, Steven C.

APPLICANT: 
                                                                                                                                            FEATURE:

OTHER INFORMATION: fusion polypeptide: hsp70(1-381)-Gly-Ser-Gly-
OTHER INFORMATION: gp100(209-217:Met210)-Gly-Ser-Gly-tyrosinase(368-376:Asp370)
US-10-328-953-330
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91.3%; Score 42; DB 15; Length 516;
Best Local Similarity 88.9%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 1; Indels
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Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELLY RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560Ale1 full length cDNA
FILLE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFUMARE: Patentin Ver. 2.1
SOFUMARE: Patentin Ver. 2.1
: LENGTH: 476
                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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; ORGANISM: Aspergillus nidulans
US-10-369-493-12366
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Best Local Similarity 88.9%;
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286 SLFEGIDFY 294
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ORGANISM: Homo sapiens
US-10-108-260A-3466
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US-10-108-260A-3466
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Db 284 SLFEGIDFY 292

Search completed: September 15, 2004, 10:51:17

Job time: 82 secs
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Sequence 14, Appl
Sequence 174, Appl
Sequence 5132, Appl
Sequence 9, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 51, Appli
Sequence 22, Appli
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Sequence 3, Appli
                                                                                                                                  September 15, 2004, 10:32:27; Search time 14.2105 Seconds (without alignments) 32.696 Million cell updates/sec
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-107-532A-1125
US-08-79-358B-3
US-08-513-783A-114
US-09-513-783A-114
US-09-134-000C-5332
US-09-107-532A-6410
US-09-343-494-9
US-09-343-494-9
US-09-107-573-2
US-08-919-573-2
US-08-919-573-2
US-08-919-573-2
US-08-919-573-2
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US-09-045-467-22
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB
                                                                                                                                                                                                                                                                              Sequence:
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                                                                                                                                    Run on:
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Sequence 5019, Ap Sequence 36, Appl Sequence 1, Appli Sequence 294, Appl Sequence 24, Appl Sequence 2, Appli Sequence 605, Appli Sequence 2, Appli	ush ID SEQUENCES RELATING TO DIAGNOSTICS AND THERAPEUTI ON
US-09-543-681A-5019 US-09-632-538C-36 US-08-727-308-1 US-08-936-165A-294 US-08-938-52-5812 US-08-43-883A-24 US-08-643-883A-24 US-08-643-883A-24 US-08-643-883A-24 US-08-645-5248-24 US-09-65-67-24 US-09-604-073-2 US-09-604-073-2 US-09-604-073-2 US-09-604-073-2 US-09-604-073-2 US-09-543-681A-8261 US-09-108-455A-605 US-09-328-352-4229 US-09-743-847-2	JGNMENTS JGNMENTS AMA and David B CID AND AMINO AC CUS FABCIUM FOR SBUTICS CORPORATI t  660 wn> 9/107,532A 85,598 51571 7 Deneke 489 GTC-012
7878 885 885 885 885 885 885 885	plication US/0910755 5 TION: Lynn A Doucette-St NVENTION: NVENTION: SERVINGES: SEGUENCES: 7310 ENERROCCE SEQUENCES: 7310 ENERROCCE SEGUENCES: 7310 ENERROCCE SEGUENCES: 7310 ENERROCCE SEGUENCES: 7310 ENERROCCE SEGUENCES: 7310 ENERROCCE THERROCCE SEGUENCES: 7310 ENERROCCE THERROCCE TING SYSTEM: 400 ENERROCCE SACII TERROCCE SACII TERROCCE SACII TERROCCE SACII TORNION DATA: 1998 CATION NUMBER: 60/0 3 DATE: 14 May 1998 CATION NUMBER: 60/0 CATION N
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	7-532A-7125 RADIALS, Application US/091075 No. 6583275 RAL INPORMATION: APPLICANT: Lynn A Doucette-St TITLE OF INVENTION: NUCLEIC A RIPEROCCO CORRESPONDENCES: 7310 CORRESPONDENCES: 7310 CORRESPONDENCES: 7310 CORRESPONDENCES: 7310 CORRESPONDENCES: 7310 COUNTRY: USA ZIRET: 100 Beaver Stree CITY: Waslaham STATE: Massachusetts COUNTRY: USA ZIP: 02354 COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM 1SO9 COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM 1SO9 COMPUTER: BCCOMPUTER: BCCOMPUTER: BCCOMPUTER: BCCOMPUTER: BCCOMPUTER: BCCOMPUTER: 30-Jun-198 PRICHING DATE: 14 May 1998 APPLICATION NUMBER: 60/0 FILING DATE: 14 MAY 1998 APPLICATION DATE: 14 MAY 1998 APPLICATION NUMBER: 60/0 FILING DATE: 14 MAY 1998
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NAME/KEY: misc feature LOCATION: (B) LÖCATION 1...226 SRQUENCE DESCRIPTION: SEQ ID NO: 7125:

US-09-107-532A-7125

6114, Ap

ORGANISM: Enterococcus faecium

ORIGINAL SOURCE:

FEATURE

LENGTH: 226 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES

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; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSC70
US-09-513-783A-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.8%; Score 39; DB 4; Length 890; 77.8%; Pred. No. 14; ive 1; Mismatches 1; Indels
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US-09-513-783A-174
; Sequence 174, Application US/09513783A
; Patent No. 6416559
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
APPLICANT: Application Kavi
; TITLE OF INVENTION: A System for Cell Based Screening
; TITLE OF INVENTION: A System for Cell Based Screening
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT APPLICATION NUMBER: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 890
                                                                                                                                                               COMPUTER: IDADY disk COMPUTER: IDADY disk COMPUTER: IDADY GISK COMPUTER: IDADY GISK COMPUTER: IDADY COMPATIBLE COMPUTER: IDADY COMPUTER: IDADY GISTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139 FILING DATE: 15-MAY-1995
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTONENTY/AGENT INPOMERTION:
NAME: DGGGGIO, Frank S.
REGISTRATION NUMBER: 31,346
             E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELERAX: 516-742-4343
TELERAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 646 amino acids
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amino acid
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Best Local Similarity 77.8
Matches 7; Conservative
                                                           CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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286 SLYEGIDFY 294
CORRESPONDENCE ADDRESS:
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                  ADDRESSEE: SCULLY,
STREET: 400 Garden
CITY: Garden City
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                 Sequence 3, Application US/08797358B
Sequence 3, Application US/08797358B
Patent No. 6268478
GENERAL INFORMATION:
APPLICANT: Adams, John
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores Lip
STREET: 470 La Johla Village Drive, Suite 700
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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MEDIUM TYBE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSTRICATION: CURROWN>
PRIOR APPLICATION NUMBER: US 60/011,491
FILING DATE: 12-FEB-1996
ATCONEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 9-CE 3165
TELECOMMUNICATION NUMBER: P-CE 3165
TELECOMMUNICATION NUMBER: P-CE 3165
TELECOMMUNICATION NUMBER: P-CE 3165
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 3; Length 643;
Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-441-139-14
Sequence 14, Application US/08441139
Sequence 14, Application US/08441139
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
NUMBER OF SEQUENCES: 20
                             Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                        0; Indels
                             Score 41; DB 4;
Pred. No. 1.2;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-797-358B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 643 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS
                                  89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.5.
Section 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 SLFEGVDFY 296
                                                                                                                                                               189 LFEGIDVY 196
                                                                                                                   2 LFEGIDIY 9
                                                                                                                                                                                                                                 RESULT 2
US-08-797-358B-3
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Gaps

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a Voltage-Gated Potassium Channel Subunit
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Sequence 11, Application US/09358383C
GENERAL INFORMATION:
APPLICANT: CLETIS, ROLY A.J.
ITILE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREPOR
FILLS REFERENCE: MNI-055CP
CURRENT FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: USSN 09/119,855
PRIOR PLICATION NUMBER: USSN 09/119,855
NUMBER OF SEQ ID NOS: 36
SOFTWARE PATENTIN Ver. 2.0
SEQ ID NO: 11
LENGTH: 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Drosophila Elk (dElk; Eag (ether a go-go)-like K+OTHER INFORMATION: gene) protein
                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·;
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                                                                                                                                                                                                               Score 35; DB 4; Length 319;
Pred. No. 28;
2; Mismatches 0; Indels
                                                                             NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...319

SEQUENCE DESCRIPTION: SEQ ID NO: 6410:
US-09-107-532A-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GREERAL INCORNATION:
APPLICANT: Jegla, Timothy J.
APPLICANT: Jegla, Timothy J.
APPLICANT: Jegla, Timothy J.
TITLE OF INVENTION: Human Elk, a Voltage-Gate
TITLE OF INVENTION: Human Elk, a Voltage-Gate
FILE REFERENCE: 018512-001320US
CURRENT APPLICATION NUMBER: US 60/91,469
EARLIER FILING DATE: 1999-06-30
EARLIER FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 9
SOUTWARE: PATENTY OF THE SEAL OF SEQ ID NOS: 9
SOUTWARE: PATENTY OF SEQ ID NOS: 9
LENGTH: 1284
HYPOTHETICAL: YES ORIGINAL SOURCE: ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-343-494-9; Sequence 9, Application US/09343494; Patent No. 6413741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT; ORGANISM: Drosophila melanogaster
US-09-358-383C-11
                                                                                                                                                                                                            h 76.1%;
Similarity 75.0%;
6; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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|126 LFQGIDIF 133
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                                                                                                                                                                                                                                  Best Local Similarity
                                                                   FEATURE:
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                                                                                                                                                                                                            Query Match
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Patent No. 6583275

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                           Sequence 5332, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: EXTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/134,000C
FILE REPERENCE: 032796-032
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
SPIOR FILING DATE: 1997-08-15
SOFTWARE: PatentIn version 3.1
SEQ ID NOS: 6812
SEQ ID NOS: 332
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Pred. No. 18;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/051571
FILING DATE: 14 May 1998
FILING DATE: 1012 2, 1997
ATTORNEY/AGDATION NUMBER: 60/051571
ATTORNEY/AGDATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6410:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.3%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.0.
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28 SIFDGIEVY 36
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    RESULT 5
US-09-134-000C-5332
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TOPOLOGY: linear US-08-919-573-4
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                                                  COUNTRY: USP
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        Score 33; DB 4; Length 1284; Pred. No. 3.2e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                             US-08-919-573-2

US-08-919-573-2

Sequence 2, Application US/08919573

Fatent No. 6346392

GENERAL INFORMATION:

APPLICANT: Burnham, Martin, Karl Russel

TITLE OF INVENTION: NOVEL GLUTAMINE TRANSPORT

TITLE OF INVENTION: ATP-BINDING PROTEIN

NUMBER OF SEQUENCES: 6

CORRESPONDENCES: 6

CORRESPONDENCES: 6

CORRESPONDENCE ADDRESSE:

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STREE: NJ

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08919573
; Patent No. 6346392
; GENERAL INFORMATION:
APPLICANT: Burnham, Martin, Karl Russel
TITLE OF INVENTION: NOVEL GLUTAMINE TRANSPORT
TITLE OF INVENTION: ATP-BINDING PROTEIN
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURTERNY EPPLICATION DATA:
APPLICATION NUMBER: US/08/919,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/ABRY INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERRICE/POCKET NUMBER: 1950597
TELEPHONE: 609-520-3214
TELEFRAX: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 244 amino acids TYPE: amino acid STRANDEDNESS: single
              71.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                  1 SLFEGIDIY 9
Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|||:||
63 IFEGVDI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LFEGIDI 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-919-573-2
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ADDRESSEE: Dechert Price & Rhoads
STREET: 1 savecevile
STREET: 997 Lenox Dive, Building 3, Suite 210
STREET: 1 savecevile
COMPTRES: 138
COMPTRES: 1880 COMPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 452;
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ZIP: 2006-1812

ZIP: 2006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,869
FILING DATE: 24-JAN-1997
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/290,978
FILING DATE: 17-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: MTGASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCS/DOCKET NUMBER: 4615-0044.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.6%; Score 32; DB 1; I
85.7%; Pred. No. 1.6e+02;
iive 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KUSTERS-VAN SOMEREN, MARGO A. MULLER, YVONNE
KESTER, HERMANUS C.M.
VISSER, JACOB
                                                                                                                               4615-0044.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: MORRISON & FOERSTER
2000 Pennsylvania Avenue N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VAN OOYEN, ALBERT J.J.
APPLICANT: ROLIN, CLAUS
TITLE OF INVENTION: CLONING AND E
TITLE OF INVENTION: EXO-POLYGALAC
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-
TELECOMMUNICATION INFORMATION:
TELERPAX: (202) 887-1500
TELERY (202) 887-1500
TELEX: 90-4030
INFORMATION FOR EGO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08780869
Patent No. 5830737
GENERAL INFORMATION:
APPLICANT: KUSTERS-VAN SOMEREN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELBEAX: (202)
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-780-869-5
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203 LFDGIDI 209
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STREET: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-290-978A-5
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-780-869-5
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Patent No. 6380370

APPLICANT: LYNORMATION:
PAPELICANT: LYND DOUGETE-Stamm et al
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1999-08-13
PRIOR PAPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PELICH DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5482
LENGTH: 722
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                                                                                                                                                                                                                        Sequence 61, Application US/09457046B
Patent No. 6287835
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
ITLE REPERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
NUMBER OF SEQ ID NOS: 74
SOFTWARE PATENT ILLING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
                                                                Gaps
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                         Length 452;
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                 69.6%; Score 32; DB 2; Length 452
85.7%; Pred. No. 1.68+02;
ive 1; Mismatches 0; Indels
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85.7%; Pred. No. 2.7e+02;
Live 1; Mismatches 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Arabidopsis thaliana
Query Match
Best Local Similarity 85.,
'.e 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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US-08-438-753B-22
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LENGTH: 458
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APPLICANT: Inakawa, Kazuhito
TITLE OP INTERNION: Interferor Teu Compositions and
TITLE OF INTERNION: Interferor Teu Compositions and
TITLE OF INTERNION: Enterferor Teu Compositions and
TITLE OF INTERNION: Enterferor Teu Compositions
CORRESPONDERS ADDRESS.
ADDRESSEE: Defilinger & Associates
GTTY: Palo Alco
GTTY: Palo Alco
GTTY: Palo Alco
GTTY: Tel Apply disk
COMPUTER FEADALE FORM:
MEDIUM TYPE: Interprive Compactible
GORFATING SUFFR: IN PC COMPACTISE
GORFATING NUMBER: US 08/139,891
FILING DATE: 10-0AY-1392
FILING DATE: 10-0AY-139
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Search completed: September 15, 2004, 10:36:49 Job time : 15.2105 secs

83 SYFQGIHIY 91

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5.1.6 Compugen Ltd. GenCore version (c) 1993 - 2004 Copyright

OM protein - protein search, using sw model

September 15, 2004, 10:29:20; Search time 47.8421 Seconds (without alignments) 53.153 Million cell updates/sec Run on:

US-09-673-795-1 46 Title:

1 SLFEGIDIY 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp1980s:\* geneseqp2002s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

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SUMMARIES	ID	AAY44199	AAB97601	ABG79108	AAY44200	AAB97602	AAB97603	ABR82812	ABM73781	ABM73972	AAY88410	AAY88413	AAY88409	AAY88412	AAB23252	AAR03930	AAR03929	AAW10065	AAY88408	AAX88411	AAB23653	4137	ANDARONA	TOO CENTER	ALM 34349	65	AAB82534
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## ALIGNMENTS

Heat shock protein 70 amino acid residues 286-294. AAY44199 standard; peptide; 9 AA. (first entry) 15-FEB-2000 AAY44199; RESULT 1 AAY44199 

Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; immune defence; immunogenicity; specificity; human leucocyte antigen.

Homo sapiens.

WO9954464-A1.

28-OCT-1999.

99WO-FR000957. 22-APR-1999; 98FR-00005033. 22-APR-1998;

(INSR ) INST ROUSSY GUSTAVE.

Gaudin C; Triebel F,

WPI; 2000-013251/01.

for treatment of Identifying mutant peptides from heat-shock protein 70, cancer.

Claim 10; Page 6; 56pp; French.

This peptide corresponds to amino acid residues 286-294 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific one mutation or alteration of the hsp70 peptides that have at least a tumour-specific response. comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) aloning the amplified encoding DNA from one or more tumours; (ii) aloning the amplified sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer,

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The amino acid sequence of fragment 1 relating to position 286-294 of
thuman heat shock protein 70 (HSP70) is given. The new invention relates
thuman heat shock protein 70 (HSP70) is given. The new invention relates
to lymphocytes which recognise cells of a patient in which overexpression
of HSP has been induced. Overexpression of HSP leads to a substantial
increase in the numbers of HSPs and HSP pitopes presented on the
pericellular membranes by lymphocytes elicits a cytotoxic
response which kills the target cells. As a further embodiment of the
invention, HSP70 epitopes are mutated prior to being loaded into antigen
to presenting cells. This has the effect of increasing the immune response
to HSP and helps direct the immune response to specific cells, (e.g.
cancer cells). HSP70 fragments are useful for treating cancer or
intracellular infections by vaccination. The tolerance of the organism to
the tumour or to the virus associated HSP is broken using an immunogenic
mutated form of HSP and induction of a stress on the target tumoural or
intracellular infected cells
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particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may also be used to increase the proportion of tumour-specific cytotoxic T lymphocytes in a cell culture and/or induce these cells to secrete cytotoxic factors (specifically interleukin-2, interferon-camma and tumour necrosis factor), particularly where the cells are used to stimulate immune defences. The method identifies peptides with high immunogenicity and high specificity for particular HLA (human leucocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSP, HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 1.
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                Length 9;
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                                                                                                                                                                                                                                            100.0%; Score 46; DB 3; L
100.0%; Pred. No. 1.4e+06;
cive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB97601 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-2000; 2000WO-EP009530.
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                                                                                                                                                                                                               Sequence 9 AA;
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The invention relates to a composition (I) comprising an immune effector cell and a cell penetrating peptide (CPP) associated with an antigen or antibody. Also included are (1) a vaccine comprising (I), CPP associated with an antigen, and a pharmaceutically acceptable carrier and (2) preparing a composition for a disease, by providing (I) and CPP associated with an antigen for disease, and introducing the antigens are, for example, tumour antigen enters into the cell. The antigens are, for example, tumour antigen exprise specialists of the antigen of the composition is useful for enhancing immunity in an animal to a disease, by administering a mature dendritic cell comprising CPP associated with an antigen to disease, to the animal comprision that following the administration, animal is protected from disease, where the animal comprises both CD4+ and CD8+ T cells. It is also useful for treating a lime.
                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma, breast cancer, prostate cancer, ovarian cancer and pancreatic cancer). The animal is further subjected to a cancer treatment including surgery, radiation, chemotherapy or gene therapy. The administration of (1), preferably dendritic cell is prior to, subsequent to or concurrent with,
                                                                                                                                                                                                                                                                                                                                                                                                            Cell penetrating peptide; cancer; tumour; melanoma; thymoma; lymphoma; leukaemia; lymphoma; leukaemia; Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel composition for treating a disease in an animal, comprises an immune effector cell and cell penetrating peptide associated with an antigen or antibody.
                                                                                Gaps
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                                            100.0%; Score 46; DB 4; Length 9; 100.0%; Pred. No. 1.4e+06;
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                                                                                                                                                                                                                                                               ABG79108 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                        Conservative
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              Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                            15-NOV-2002
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identifying mutant peptides from heat-shock protein 70, for treatment of
                                                                                                                                                                                                                    Human; heat shock protein 70; hsp70; identification; tumour; mutation; 
T cell response; amplification; vector; bacterium; cancer; allele; 
cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; 
immune defence; immunogenicity; specificity; human leucocyte antigen.
the cancer treatment. The present sequence is a tumour antigen derived epitope for inclusion in the composition of the invention
                                                 Length 9;
                                                                 Indels
                                             ; Score 46; DB 5; Le
; Pred. No. 1.4e+06;
0; Mismatches 0;
                                                                                                                                                                                                  Heat shock protein 70 amino acid residues 286-295.
                                                                                                                                              AAY44200 standard; peptide; 10 AA.
                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 6; 56pp; French.
                                                                                                                                                                                                                                                                                                                         99WO-FR000957,
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                                                                                                SLFEGIDIY
                                                      Best Local Similarity
                                                                                 1 SLFEGIDIY
                           Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                       22-APR-1999;
                                                                                                                                                                                                                                                                   Homo sapiens
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This peptide corresponds to amino acid residues 286-295 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response, comprises: (i) amplifying hsp70 concorred into a vector that can be replicated in bacteria; (iii) coning the amplified sequences into a vector that can be replicated in bacteria; (iii) containing fragments in each cultured bacterial colony to identify any epytides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer, cancers of head and neck, particularly kidney cancer). The peptides may cancers of head and neck, particularly kidney cancer). The peptides may lymphocytes in a cell culture and/or induce these cells to secrete cytotoxic factors (specifically interleutin-2, interferon-gamma and cytomour necrosis factor), particularly where the cells are used to immunogenicity and high specificity for particular HIA (human leucocyte

Sequence 10 AA;

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The amino acid sequence of fragment 2 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to 1ymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP pitopes presented on the pericellular membranes. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic invention, HSPN epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSPVO fragments are useful for treating cancer or intracellular infections by vaccinated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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                                                                                                                                                                                                                                                                                                               HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 2.
                                                         Gaps
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                   100.0%; Score 46; DB 3; Length 10; 100.0%; Pred. No. 0.0086;
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                                                    0; Indels
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                                                     Mismatches
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                                                                                                                                                                                        AAB97602 standard; peptide; 10 AA.
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                                                  Conservative
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Query Match
Best Local Similarity
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Best Local Similarity
Matches 9; Consery
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RESULT 6 AAB97603

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Human hsp70 peptide p20 (residues 286-305).
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Matches 8; Conservative
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                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSEP70) is given. The new invention relates human heat shock protein 70 (HSEP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes or call pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or infractions by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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                                                                                                                                                                                                         HSP, HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 3.
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88.9%; Pred. No. 0.058;
iive 0; Mismatches 1; Indels
                                                                                                                                                                         Heat shock protein 70 (HSP70) peptidic fragment 3.
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                                                                        AAB97603 standard; peptide; 10 AA
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intracellular infected cells
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Best Local Similarity
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RESULT 7 ABR82812

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Sarley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
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Heat-shock protein 70; hsp70; antidiabetic; human; immunosuppressive; dermatological; antiinflammatory; neuroprotective; antirheumatic; antiarthritic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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(YEDA ) YEDA RES & DEV CO LTD.
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The present invention relates to oligonucleotide clones originating in barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonucleotide clone sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fite, wipo.int/pub/published-pct-sequences
                                                                                                                                                                                                                          Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of barley varieties and production of barley transformants with desired
                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID XX; 284pp; Japanese.
20-DEC-2001; 2001JP-00387131.
20-DEC-2001; 2001JP-00403299.
20-DEC-2001; 2001JP-00403300.
27-SEP-2002; 2002JP-00327515.
                                                                                                                                                  Kohara Y;
                                                                                                     (UYNI-) UNIV JAPAN OKAYAMA.
                                                                                                                                                                                    WPI; 2003-587127/55
                                                                                                                                                Takeda K,
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          Score 42; DB 7; Length 438;
Pred. No. 3.6;
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        91.3%;
88.9%;
Query Match
Best Local Similarity 88.20,
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SLFEGIDEY 300

292

g G

DNA clone originating in barley containing SNP sequence #382. ABM73972 standard; protein; 454 AA. (first entry) 17-0CT-2003 ABM73972; RESULT 

Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.

Hordeum vulgare

WO2003057877-A1

16-DEC-2002; 2002WO-IB005403 17-JUL-2003

20-DEC-2001; 2001JP-00387111. 20-DEC-2001; 2001JP-00403299. 20-DEC-2001; 2001JP-00403300. 27-SEP-2002; 2002JP-00327515. 2001JP-00387059 20-DEC-2001;

(UYNI-) UNIV JAPAN OKAYAMA.

Takeda K, Sato K,

WPI; 2003-587127/55

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DNA
barley
Single nucleotide polymorphism sites in barley varieties and I sequences containing them for analysis and identification of Nazieties and production of barley transformants with desired characteristics.
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Disclosure, SEQ ID XX; 284pp; Japanese.

The present invention relates to oligonucleotide clones originating in barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype transformation of specific genes and creation of new varieties by varieties with desired properties. The present sequence represents an oligonucleotide clone sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip, wipo.int/pub/published-pct-sequences 

Sequence 454 AA;

Gaps ö 7; Length 454; 1; Indels DB 7 Score 42; DB 7 Pred. No. 3.8; 0; Mismatches 0; 91.3%; 8; Conservative Local Similarity Query Match Matches

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156 σ 1 SLFEGIDIY SLFEGIDEY 148

à 원

AAY88410 standard; protein; 554 AA. (first entry) 31-JUL-2000 AAY88410; RESULT 10 

Human heat shock protein SHSP70 amino acid sequence.

Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70. Human;

Homo sapiens

JP2000069999-A.

07-MAR-2000

99JP-00257146 01-JUN-1995;

(HOKE-) HOKEN KAGAKU KENKYUSHO KK. 95JP-00158581

01-JUN-1995;

2000-264458/23

N-PSDB; AAA15622

Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application,

Disclosure, Fig 3; 11pp; Japanese.

This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 1462-2-4. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome

Sequence 554

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Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
                                                                                                                                                                                                                                                                                                               Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome
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chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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0; Mismatches
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88.9%;
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Best Local Similarity 88.5
Matches 8; Conservative
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                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
                                                                                                                                                                                                                                                                                                                                                           Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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                                Length 554;
                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human heat shock protein SHSP70 amino acid sequence
                                                                                                                                                                                                                                                                                                                            Human heat shock protein SHSP70 amino acid sequence.
                                  DB 3;
                                Score 42; DB 3
Pred. No. 4.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY88409 standard; protein; 554 AA.
                                                                                                                                                                                                                           AAY88413 standard; protein; 554 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 6; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HOKE-) HOKEN KAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-00257146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95JP-00158581
                                   91.3%;
88.9%;
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                 Query Match
Best Local Similarity
8; Conserve
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les 8; Conserv
                                                                                                    1 SLFEGIDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP2000069999-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2000
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AXAXAXXXXXX

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Gaps

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the proliferation of cells. Modulation of the activity of the JNK phosphatase or Hsp72 is used to treat a proliferative disorder such as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 activity can also be administered to treat premalignant conditions and to prevent progression to a neoplastic or malignant state. The compounds that inhibit Hsp72 function are administered to a patient having a disease or disorder mediated by an increase of Hsp72 expression or activity relative to normal levels. The present sequence represents human Hsp72 used in the exemplifications of the invention

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Gaps

0;

Length 624; Indels

Score 42; DB 3; Pred. No. 5.3; ); Mismatches

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Conservative

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Sest Local Similarity

Query Match Matches

Sequence 624 AA;

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1 SLFEGIDIY

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286 SLFEGIDFY 294

91.3%; 88.9%;

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                    This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome
                                                                                                                                                                                                                                                                                                                                                             Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.
                                                                                                                                                                    Gaps
                                                                                                                                                                   0;
                                                                                                                                        Score 42; DB 3; Length 554;
Pred. No. 4.7;
                                                                                                                                                                  1; Indels
                                                                                                                                                      Pred. No. 4.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                         (heat shock protein 72).
                                                                                                                                                                                                                                                                  AAB23252 standard; protein; 624 AA.
Disclosure; Fig 5; 11pp; Japanese.
                                                                                                                                         91.3%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-2000; 2000WO-US007350.
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                          200 SLPEGIDEY 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Volloch VZ, Sherman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PHYL-) PHYLOGENY INC.
                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-647056/62.
                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                     1 SLFEGIDIY
                                                                                                                 Sequence 554 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                         Human Hsp72
                                                                                                                                                                                                                                                                                                                  29-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000.
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                                                                                                                                                                                                                                              RESULT 14
AAB23252
8 X C C C C C C C X S
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AAR03930 standard; protein; 634 AA.

RESULT 15

AAR03930

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According to the legend of Fig 2, the G. gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "O" (?) at position 634. Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M. hyopneumoniae (Mnyhspy0 - AAR03922); 2. Bacillus megaterium (Bmehspy0 - AAR03923); 3. E. coli (dnaK - AAR03924); 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus (rathspy0 - AAR03925); 9. Gallus gallus (chkhspy0 - AAR03930); 10. Zea mays (mzehspy0 - AAR03931); 11. Serratia marcescens (smahsp70 - AAR03932); 7. AAR03932); 11. Serratia marcescens (smahsp70 - AAR03932); avecines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                                                                                                                                                                                                                                                                                                                                                             Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2.1-2.14; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                          Sias S;
                                                                                                                                                                                                                                                                                                                 88US-00243474
                                                                                                                                                                                                                                                                                                                                                                        Dragon E, Faulds D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacteria species
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-115820/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 634 AA;
                                                                                                                                                                                                                                                                                                                                            (CODO-) CODON
                                                                                                                                                                                                                                                                                                                12-SEP-1988;
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The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a cell which overexpresses Hsp72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of Hsp72.

Optionally, Hsp72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp72-mediated JNK phosphatase activation, comprising contacting a test compound with a cell which determining if the compound inhibits JNK phosphatase activity. The invention additionally encompasses compositions compressing an inhibitor of Hsp72 or JNK phosphatase activity. The compounds identified as inhibitors of Hsp72 or JNK phosphatase activity are useful for inhibiting

Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia, lymphoma.

Example, Fig 16B, 77pp, English.

/note= "residue given as "O" in specification"

88US-00243474.

12-SEP-1988;

Location/Qualifiers

Misc-difference

WO9002564-A. 22-MAR-1990

Gallus gallus.

Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

Gallus gallus HSP (chkhsp70).

30-AUG-1990 (first entry)

AAR03930;

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Query Match 91.3%; Score 42; DB 2; Length 634; Best Local Similarity 88.9%; Pred. No. 5.4; Matches 8; Conservative 0; Mismatches 1; Indels
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0; Gaps

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Search completed: September 15, 2004, 10:34:08 Job time: 50.3421 secs